

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 113875

TO: Minh-Tam Davis

Location: Rem 3a24 / 3c18 Tuesday, February 10, 2004

Art Unit: 1642 Phone: 272-0830

Serial Number: 10 / 017066

From: Jan Delaval

**Location: Biotech-Chem Library** 

**Rem 1A51** 

Phone: 272-2504

jan.delaval@uspto.gov

### Search Notes

muty date 10/2000 10/1999

Getta seul requeted 02/18/04



#### STIC-Biotech/ChemLib

From:

Chan, Christina

Sent:

Monday, February 09, 2004 2:09 PM

To:

Davis, Minh-Tam; STIC-Biotech/ChemLib/

Subject:

RE: Rush search request for 10/017066

#### Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Monday, February 09, 2004 12:11 PM

To:

Chan, Christina

Subject:

Rush search request for 10/017066

Please search in commercial database, issued patent files, PGPUB and for interference: SEQ ID NO:1 and 2.

Thank you.

MINH TAM DAVIS

ART UNIT 1642

RESEM, ROOM 3A24, MB 3C18

272-0830

Searcher:	Ja
Phone:	22504
Location:	
Date Picked Up:	219
\Date Completed:_	2100
'Şearcher Prep/Rev	/iew:
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TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

CONTONE OF	FEB 19 2004	RECEIVED

G Z
VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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RESULT 14
US-09-016-434-1363
                                                                                                                                                                    Sequence 1363, Application US/09016434

Sequence 1363, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Jenice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS: 1490

CORRESPONDENCE INCYTE PHARMACEUTICALS, INC.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                            STREET:
                                                                                                    COUNTRY:
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US-09-016-434-1363
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AMME: Zeller, Karen J.
REGISTRATION NUWBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1363:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local (
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TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: GENBAN
CLONE: g425220
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                          TTGCTGAGGATGGCATGTTCCAACATTCAGATTAATCACACAGTGCTGATTGCCACAGGC
                                                                                             GTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGTCATC
                                                                                                                                     AAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACCAAGAT 687
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Pred. No. 1.9e-19;
0; Mismatches 453;
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NUMBER OF SEQ ID NOS: 575

SOUTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 352
LENGTH: 251
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-352
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US-09-499-313-352/c
US-09-499-313-352/c
Sequence 352, Application US/09439313
Patent No. 6329505
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Best Local Similarity 66.0%;
Matches 163; Conservative (
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APPLICANT: DAY, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILLING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1723 ACACCCATGATGAATCCCTTCATCTACAGCCTGAGGAACAAGGACATGC 1771
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                                                                                                                                         356 TCTCCACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCC 415
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Retter, Mark
Solk, John
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Reed, Steven G.
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Pred. No. 3.8e-18;
0; Mismatches 84
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Search completed: February 9, 2004, 16:13:40 Job time : 169 secs

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Result
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpna/US10B_FUBCOMB.seq:*
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7 US-10-295-027-872
7 US-09-759-143-917
7 US-09-822-827-917
7 US-09-895-793-917
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7 US-10-144-678A-917
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7 US-10-294-025-917
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## ALIGNMENTS

US-10-001-469-2879

GENERAL INFORMATION:

Sequence 2879, Application US/10001469 Publication No. US20030091562A1

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APPLICANT: JAKOBOVITS, AYA
APPLICANT: RAITANO, ARTHUR
APPLICANT: RAFR, DANGEL
APPLICANT: SAFRA, DOUGLAS
APPLICANT: AFAR, DANGEL
APPLICANT: AFAR, DANGEL
APPLICANT: FARRS, MARY
APPLICANT: FARRS, MARY
APPLICANT: CHALLITA-EID, PIA
TITIE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITIE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITIE OF INVENTION: OLIPSAIL USEFUL IN TREATMENT AND DETECTION OF CANCER
TITIE OF INVENTION: OLIPSAIL USEFUL IN TREATMENT AND DETECTION OF CANCER
TITIE OF INVENTION: OLIPSAIL USEFUL IN TREATMENT AND DETECTION OF CANCER
TILE REFERENCE: 51158-20024-20
CURRENT FILLING DATE: 2002-0-5
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR APPLICATION NUMBER: 60/291,118
PRIOR APPLICATION NUMBER: 60/291,118
PRIOR APPLICATION NUMBER: 09/680,728
PRIOR FILING DATE: 2001-0-5
PRIOR APPLICATION NUMBER: 09/680,728
PRIOR FILING DATE: 2001-0-5
PRIOR FILING DATE: 2001-0-5
PRIOR FILING DATE: 2001-0-9
PRIOR P
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ACAAAGGAGATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAG 1080	TTGGCCAATATCTATCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATGGAGTGAAG 1020	ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATC 960	AAGGCATTTGGCACTTGCGTCTCCATGTGTGTGTGTGTTGTATATTTCTATGTACCTTTC 900	CCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCC 840	AATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATC 780	CCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTC 720	CTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATACCTT 660	GTACTTACGTTGCCTCGTGTCACCAAAATTGGTGGCTGGC	CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACA 540	GATGOTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG 480	CCTCATCCATGCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTT 420	CTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCC 360	TACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGC 300	ATAGGCCTCCCTGGTTTAGAAGAGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTC 240	AGCTTCTTCATGATGGTGGATCCCAATGGCAATGACATCCAGTGCTACATACTTCATCCTA 180	GGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCCTG	CAGAGAGGCTGTAITTCAGTGCAGCCTGCCAGACCTCTTCTGGAGGAAGACTGGACAAAG 60	3136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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TLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND
TLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TLE OF INVENTION: THERAPY OF PROSTATE CANCER
TLE OF INVENTION: THERAPY OF PROSTATE CANCER
TLE REFERENCE: MRI-044
REENT APPLICATION NUMBER: US/10/205,823
RRENT FILING DATE: 2002-07-25
IOR FILING DATE: 2001-07-25
IOR APPLICATION NUMBER: 60/314,356
IOR APPLICATION NUMBER: 60/314,356
IOR FILING DATE: 2001-08-2
IOR APPLICATION NUMBER: 60/325,020
IOR APPLICATION NUMBER: 60/341,746
IOR APPLICATION NUMBER: 60/341,746
IOR APPLICATION NUMBER: 60/341,746
IOR APPLICATION NUMBER: 60/362,158
IOR FILING DATE: 2001-12-12
IOR APPLICATION NUMBER: 60/362,158
IOR FILING DATE: 2001-08-25
IOR APPLICATION NUMBER: 60/362,158
IOR FILING DATE: 2001-12-12
IOR APPLICATION NUMBER: 60/362,158
IOR FILING DATE: 2002-03-05
MBER OF SEQ ID NOS: 455
INDEED OF SEQ ID NOS: 455
INDEED OF SEC ID NOS: 455
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RAL INFORMATION:
LICANT: Schlegel, Robert
LICANT: Schlegel, Robert
LICANT: Monahan, John E.
LICANT: Bndege, Wilson O.
LICANT: Garnavarapu, Manjula
LICANT: Gorbatcheva, Bella
LICANT: Hoersch, Sebastian
LICANT: Kamatkar, Shubhangi
LICANT: Wonsey, Angela M.
LICANT: Wonsey, Angela M.
LICANT: Glatt, Karen
LICANT: Zhao, Xumei
LICANT: Anderson, Dustin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 442
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VISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGC
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                                              GATGCTTGTCTGCTACAGATTTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG
                                                                                                                                                                                                                                                                                                               CTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCC
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                                                                                                                                                       ACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTT
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1381 TGAGATAGAATGGTACATCTAGAACATTGCCAAAGGCCTAAGCACGGCAAAGGAAA 1440 1381 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAA 1440 1381 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAA 1440 1441 ATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAG 1500 1441 ATAAACACAGAATATAATAAAATGAGATAATCTTAGCTTAAAACTATAACTTCCTCTCCAG 1500 1501 AACTCCCAACCACATTGGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAA 1560	261 TGTTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTT  261 TGTTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTT  321 CTTTTCATTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGG  321 CTTTTCATTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGG  321 CTTTTCATTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGG	081 CCCTAGGTGTCAGTGATCAAACTTCTTTTCCATTAAAAATTAATT	102 102 108 108	901 ATTGGATTGTCATGGTGATCTTAGCAAGCGGCGTGACTCTCCGCTGATCTACTATGTACCTTTC 960 901 ATTGGATTGTCATGGGATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGACTCTATC 901 ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATC 960 901 ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGACCCGTCATC 960	721 AATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATC 780  721 AATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATC 780  721 AATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATC 780  781 TCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCC 840  781 TCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCC 840	481 CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGCGCCATGCGCCATGCCACACA 540 481 CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACA 540 541 CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTGCACCCACTGCGCCATGCCACA 540 541 GTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGTGGTGGGGGGGG
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1201 GATECTTCAPATATGAPACTGGTTGGGGAATCTCCATTTTTCAPATATATTTTTTTTTT	dg dg	Qy 121 AGCTTCTTCATGATGGTGGATCCCAATGGCAATGATCCAGTGCTACATACTTCATCCTA 180
141	, B &	Oy 61 GGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCTGGTGGTGGTCACACAGTTC 120 [
9 10 1	) B 8	OY  1 CAGAGAGGCTGTATTTCAGTGCAGCCTGCCAGACCTCTTCTGGAGAAAACTTGGACAAAG 60
21	S B 8	Query Match 100.0%; Score 3136; DB 15; Length 3136; Best Local Similarity 100.0%; Pred. No. 0; Matches 3136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
961 TTGGCCAATATCTATCTGGTGGTTCCTCCTGTGCTCAACCCAATTGTCTATGGAGTGAAG 	B &	; LENGTH: 3136; ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-225-567A-433
901 ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATC 960	Qy Qy	; PRIOR FILING DATE: 2000-12-19; NUMBER OF SEQ ID NOS: 2292; SOFTWARE: Patentin version 3.1; SEQ ID NO 433
841 AAGGCATITGGCACTTGCGTCTCTCATGTGTGTGCTGTGTTCATATTCTATGTACCTTTC	dd Qy	367A
781 TCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCC	D Qy	Joseph P. Glenna C. Christine ANTIGENIC
721 AATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATC	d dd VQ	Sequence 433, A Publication No. GENERAL INFORMA APPLICANT: Lif
661 TCCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTC	Db Qy	5672-433
601 CTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTT	P 65	Qy 3121 AAAAAAAAAAAAA 3136              Db 3121 AAAAAAAAAAAA 3136
	) B 5	Cy         3061 ARARTARAGTACTATTGTGTCARGARARARARARARARARARARARARARARARARARAR
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	}	OY 2941 AGCTATGTGTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGA 3000
	· ?	OY 2881 CTGGCTCATAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGA 2940
	B &	Qy 2821 TIATTAAATTCTGGCCATTACTTCCAATGTGAGTGGAATGTGACATGTGCAATTTCTATAC 2880
	}	OY 2761 TGATTCCTTCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTA 2820
	} Db !	QY 2701 AGCAAAGTGCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACC 2760
181 ATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTC	8	Db 2641 TATTATTGAATGTCATCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCCC 2700

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2101 TICAGAAAGTCTGCATAGGGCTTATAGCAAGTTATTTATATATA	1561 GAARIAATTTTTCCTCTGGACACTTAAGGGAAATTGGAAGTAAACCTTGAA 1561 GAAATAATTTTTCCTCTGGACACTTGACGACAATTGGAAGTAAACCTTGAA 1620 1621 AAGAGTACATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAAGGCTTGAA 1620 1621 AAGAGTACATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCA 1680 1681 TATGGACCCTGTTTTTCCTAATTAATTTTCTTATCACACCTGTTCTGAGAGTTTTCACACCA 1681 TATGGACCCTGTTTTTCCTAATTTAATTTTCTTATCACCACCTGTTCTAATTAGGCAAAGATATT 1740 1681 TATGGACCCTGTTTTTCCTAATTTTAATTTTCTTATCACCCTTTAATTAGGCAAAGATATT 1740 1741 ATTAGTACCCTCATTGTAGCCATGGGAAAATTGATGCACACCTTTAATTAGGCAAAGATATT 1740 1741 ATTAGTACCCTCATTGTAGCCATGGGAAAATTGATGCACACCTTTAATTAGGCAAAGATATTAA 1800 1801 TGGGGTCATACAAGTATAAAAATTAAAAAAAAAAAAAAA	261 TGTTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTGTGGAGGGTTATTA 13 261 TGTTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTA 13 261 TGTTTTCTTTGCTACATATAATTATTAATACCCTGACTAGGTTGTAGGTTGGAGGGTTATTA 13 261 TGTTTTCATTTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTC 13 321 CTTTTCATTTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGGATTC 13 321 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAACCTGAGAGAAAAA 14 321 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCCATGGCAAAGGAAA 14 321 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAAGGCCTAAGCACGGCAAAGGAAA 14 321 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAAGGCCTAAACTTTAAACTTTCTTCTACAGGAAA 14 321 TGAGATAAGAATGAATAAAAATGAGATTAATTAAAACTATAAAACTATAAAACTATAAAACTATAAAAATGAATTAAAAATGAATTAAAAATTAAAAATGAATTAAAAATTAAAAATGAATTAAAAATTAAAAATGAATTAAAAATTAAAAATGAATTAAAAATTAAAAATGAATTCTAAAAATTAAAAATTAAAAAATGCTGTCTCAAAAATTAAAAATTAAAAAATGAATTCTAAAAATTAAAAATTAAAAAATGCTGTCTCTAAAAATTAAAATTAAAAAATGAATTCTAAAAATTAAAAATTAAAAAATGCTGTCTCAAAAATTAAAAATTAAAAAAATGCTGTCTTCAAAAATTAAAATTAAAAAAATGCTGTCTTCAAAAATTAAAAATTAAAAAAAA
RESULT 4  US-10-295-027-872  ISequence 872, Application US/10295027  Sequence 872, Application US/10295027  Publication No. US20030232350A1  GENERAL INFORMATION:  APPLICANT: Afar, Daniel APPLICANT: Ginsberg, Wendy M. APPLICANT: Gish, Kurt C. APPLICANT: Glsh, Kurt C. APPLICANT: Hevezi, Peter A. APPLICANT: Mack, David H. APPLICANT: Murray, Richard APPLICANT: Watson, Susan R. APPLICANT: Watson, Susan R. APPLICANT: Eos Biotechnology, Inc. ITILE OF INVENTION: Methods of Screening for Modulators of Cancer	2641 TATTATTGAATGCCTAGAACATTAATAGTCATTGACTGTTTTCCATCAAACCCCCCCC	Db 2341 GCAATCTGACTTAGGCATTCGACAGGATATTTTCCTTTTCGAGGGCCCATGAGACTCAAACTTAC 2460  Qy 2401 TTAATAGGTTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTAC 2460  Db 2401 TTAATAGGTTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTAC 2460  Qy 2461 AAATACTAAAACATGTATCATATATGTGGTAAGTTTCATTTTCTTTTTCAATCCCAAGGC 2520  Qy 2461 AAATACTAAAACATGTGATCATATATGTGGTAAGTTTCATTTCTTTTTCAATCCTCAGG 2520  Db 2461 AAATACTAAAACATGTGATCATATATGTGGTAAGTTTCATTTCTTTTCAATCCTCAGG 2520  Qy 2521 TTCCCCTGATATGGATTCCTATAACATGCTTTCATCCTCTTTGTAATGGATATCATATTT 2580  Db 2521 TTCCCCTGATATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATTT 2580  Qy 2581 GGAAATGCCTATTTAATACTTGTATTTGCTGCTGGTAAGCCCATGAAGGGCACTGTT 2640  Qy 2641 TATTATTGAATGCTATTTAATACTTGTATTTGCTGCTGGACTGTTAAGCCCATGAAGGCACTGTT 2640  Qy 2641 TATTATTGAATGTCATCTTGTATTTGCTGCTGTTAAGCCCCATGAAGGCACTGTT 2640  Qy 2641 TATTATTGAATGTCATCTTGTTTCATTCATTTGCTTGCTT

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2641 TATTATTGAATGTCATCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCC 2700	2581 GGAAATGCCTATTTAATACTTGTATTTGCTGCTGGACTGTAAGCCCATGAGGGCACTGTT 2640	2521 TTCCCTGATATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATAATTT 2580	2461 AAATACTAAAACATGTGATCATATATGTGGTAAGTTTCATTTTCTTTTTCAATCCTCAGG 2520 	2401 TTAATAGGTTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTAC 2460 	2341 GCAATCTGACTTAGGCATGGGAATCAGGCATTTTTGCTTCTGAGGGGGCTATTACCAAGGG 2400 	2281 AGGACCATGCTTTATTTGGGGCTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAA 2340	2221 TCTTGAAGATAACATTGGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGGAATCTTC 2280 	2161 TTCTGATAGGCAGTGAGGTTAGGGAAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGG 2220 	2101 TTCAGAAAGTCTGCATAGGGGCTTATAGCAAGTTATTTAT	2041 GCCAATTACCTÖTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTA 2100 	1981 CTGGCAACAGAACTCATGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATT 2040 	1921 ATTTICTAGAGGAGGIATTTAATTTCTTCTCACTCATCCAGTGTTGTATTTAGGAATTTC 1980	1861 TGTGGAAGAACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTAC 1920 	1801 TGGGGTCATACAAGTATAAAAATTAAAAAAAAAAAAAGACTTCATGCCCAATCTCATATGA 1860 	1741 ATTAGTACCCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAA 1800 	1681 TATGGACCCIGTTTTTCCTATTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATT 1740	1560 GAAATAATTTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAA 1619 1621 AAGAGTACATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCA 1680
CY 1149 TITIGGAAGACAGIATICAGAAAAAAATTICCTTAATAAAAAATACAACTCAGATCCTTC 1208	1089 GTCAGTGATCAAACTTCTTTTCCATTCAGATTCAGATTCAGATTTTAACGTTAACAT	1029 GATTGACAGGGCATCCTTGACTTTTCCAGGGCCACACAGGCTTCAGAGCCTAGGT	Query Match 64.7%; Score 2028.4; DB 9; Length 2061; Best Local Similarity 99.8%; Pred. No. 0; Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps	-	SEQ ID NO 917  LENGTH: EASTSEQ for Windows Version 3.0  SEQ ID NO 917  LENGTH: 2061	427C23 IBER: US/09/759,143	APPLICANT: Stelly, Yasir A.W. APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	APPLICANT: Vedvick Thomas S. APPLICANT: Vedvick Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel	APPLICANT: MAIOS, MICHAEL D.  APPLICANT: Retter, Marc W.  APPLICANT: Stolk, John A.  APPLICANT: Stolk, John A.	APPLICANT: MITCHAM, JENNIET L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqui APPLICANT: Henderson, Robert A.	; PALENT NO. USZ020022248A1 ; GENERAL INFORMATION; ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C.	RESULT 5 US-09-759-143-917 ; Sequence 917, Application US/09759143	Oy 2941 AGCTATGTGTTACACAGAGTAAATCACC 2968	2881 CTGGCTCATAAAACCCTCCCATGTGCAG	2821 TTATTA-ARTTCTGGCCATTACTTCCA-ATCTGA-GTGGA-ACTGGA-CATGTGCA-ATTTCTATAC	2761 TGATTCCTTCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTA	2701 AGCA      2698 AGCA

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2049 CCTGTGTCTTGGAAGAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA 2108 1020 CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATTGGAAGATTCTTATTCAGAAA 1079 2109 GTCTGCATAGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA 2168 1080 GTCTGCATAGGGCTTATAGCAAGTTATTTATTTTAAAAGTTCCATAGGTGATTCTGATA 1139 2169 GGCAGTGAGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA 1139 2169 GGCAGTGAGGGTTAGGGAGCCACCAGTTATGGAAGGTAGGAATGGGAAGGTCTTGAAG 2228 1140 GGCAGTGAGGTTAGGGAAGCCACCAGTTATGGAAGGTATGGGAATGGGAAGGTCTTGAAG 1199 2229 ATAACATTGGCCTTTTGAAGTGTGACTCGTAGGAAGTGAGGAATCTTCAGGACCAT 2288 1141   GCCAGTTGGCCTTTTGAAGTGTGACTCGTAGGAAGTGAGGGAATCTTCAGGACCAT 2288 1200 ATAACATTGGCCTTTTGAAGTGTGACTCGTAGGAAGTGAGGGAATCTTCAGGACCAT 1259 2289 GCTTTATTTGGGGGCTTTTGAGTGAACTGGGAAAGTGAGGGAATCTTCAGGACCAT 1259	1209 ANATATGAANCTGGTTTGGGGAATCTCCATTTTTCANTATTATTTTCTTTTC
RESULT 6 US-09-780-669-917 US-09-780-669-917, Application US/09780669 Sequence 917, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION: APPLICANT: Mutcham, Jennifer L. APPLICANT: Mitcham, Jennifer L. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S.	Db 1260 GCITIANTINGGGCCTITIGTCCAGGIACTGGGGCCATTTTTGAGACCAGGAAAGCAATTTG 1119  2319 ACTTAGGATGGGAATCAGGCATTTTTGCTTCTGAGAGCCAGGAAAGCAATTTG 1119  2409 TTCATCTTCAACAGGATATCAGCATTTTTGCTTCTTGAGAGCCAGGAAAGCCAATTACTAA 2469  2409 TTCATCTTCAACAGGATATCAGCATTTTTGCTTTCTTTTCATACCAAGGTTAATACTAA 2469  2409 TTCATCTTCAACAGGATATCAGCATTTTCATTTCTTTTCATACCAAGGTTAATACTAA 2469  2409 TTCATCTTCAACAGGATATCAGCATTTTCCTTTTCATACCAACTTCAAATACTAATACTAATACTAATACTAATACTAATACTAACTACAAAAACCCAAAAACCCAAAAACCCAAAAACCCAAAAACCCAAAA

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APPLICANT: Mang, Asjum
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 917
LENGTH: 2061
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-917
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Best Local Similarity
Matches 2052; Conserv
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                                          CTGTTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTAC
                                                                                                                                                                     TTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCCTTGAAAAGAGTAC
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QY 1449 AGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA	Qy 1389 GAATGGTACATCTAGAGAACATTTGCCAAAAGGCCTAAGCACGGCAAAGGAAAATAAACA	QY 1329 TTTACCATGCAGAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAA	Qy 1269 TGCTACATATAATTAATTACCCTGACTAGGTTGGTGGTGGAGGGTTATTACTTTTCA	Qy 1209 ABATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTTTTT	Qy 1149 TTTGGAAGACAGTATTCAGAAAAAAATTTTCCTTAATAAAAAATAACAACTCAGATCCTTC	Qy 1089 GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT	QY 1029 GATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCCTTCAGAGCCCTAGGT	Query Match Best Local Similarity 99.8%; Pred. No. 0; Matches 2052; Conservative 0; Mismatches	; LENGTH: 2061 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-822-827-917	; CURRENT FILING DATE: 2001-03-28 ; NUMBER OF SEQ ID NOS: 982 ; SOFTWARE: FASTSEQ for Windows Version 3.0 ; SEQ ID NO 917	: TITLE OF INVENTION: COMPOSITIONS AND METHODS I : TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAN : FILE REFERENCE: 210121.534C1 : CURRENT APPLICATION NUMBER: US/09/822,827	; Sequence 917, Application US/09822827 ; Patent No. US20020081680A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun	RESULT 7 US-09-822-827-917	Qy 3069 GTACTATTGTGTCAAG 3084	Qy 3009 TCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAAAATAAA	2949 GTTACACAGAGTAAATCACCAGAAGCCTGGATTT	Qy 2889 TAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCTATGT	
	TAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACAC 1448 .	QATGGTTTACAGCATTCTGAGATAA 1388	T 1328	1268	1208	1148	T 1088	DB 9; Length 2061; 1; Indels 3; Gaps 2;			S FOR THE THERAPY AND CANCER				3068	C 3008	2948	1859
7 2529 TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATTTGGAAATGC 2588	7 2469 ANACATGTGATCATATGTGGTAAGTTTCATTTTCTTTTTCAATCCTCAGGTTCCCTGA 2528	1380	2349 ACTTAGGCATGAGAATCAGGCATTTTTGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG 240	2289 GCTTTATTTGGGGCTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAAGCAATCTG	QY 2229 ATAACATTGGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGAATCTTCAGGACCAT 2288	2169 GGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGGTCTTGAAG 2	QY 2109 GTCTGCATAGGGCTTATAGCAAGTTATTTATATTTTTAAAAGTTCCATAGGTGATTCTGATA 2168	Qy 2049 CCTGTGTCTTGGAAGAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA 2108	Qy 1989 AGAACTCATGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTA 2048	Qy 1929 GAGGAGGTATTTAATTTCTTCTCACTCATCCAGTGTTGTATTTAGGAATTTCCTGGCAAC 1988	Qy 1869 AACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 1928	QY 1809 TACAAGTATAAAAATTAAAAAAAAAAAAAAAAAAAAAAA	QY 1749 CCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGATCAGTGAATTAAATGGGGTCA 1808	OY 1689 CTGTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTAC 1748	1629 ATTTACCTACGTTARGARAGTTGACACACTGTTCTGAGAGTTTTCACACACATATGGACC	N G	1509 482	422 AGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA

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RESULT 8
US-09-895-793-917
; Sequence 917, App.
; Publication No. 1
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C2

CURRENT APPLICATION NUMBER: US/09/895,793

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 917
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Vedvick, Thomas S.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Stolk, John F
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ITITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER.
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 917
SEQ ID NO 917
LENGTH: 2061
TYPE: DNA
GRAANISM: Homo sapiens
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APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Btolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
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Best Local Similarity
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McNeill, Patricia D.
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Hepler, William T.
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RESULT 10  US-10-144-678A-917  Sequence 917, Application US/10144678A  Publication No. US20030157089A1  GENERAL INFORMATION:  APPLICANT: Xu, Jiangchun  APPLICANT: Harlocker, Susan L.  APPLICANT: Harlocker, Susan L.  APPLICANT: Handerson, Robert A.  APPLICANT: Kalos, Michael D.  APPLICANT: Retter, Marc W.  APPLICANT: Stolk, John A.  APPLICANT: Stolk, John A.  APPLICANT: Vedvick, Thomas S.  APPLICANT: Vedvick, Thomas S.  APPLICANT: Us, Samuel X.  APPLICANT: Hang, Aijun  APPLICANT: Hang, Aijun  APPLICANT: Henger, William T.  APPLICANT: Henger, William T.  APPLICANT: Houghton, Raymond L.  APPLICANT: Houghton, Raymond L.  APPLICANT: Houghton, Raymond L.  APPLICANT: Houghton, Raymond L.  APPLICANT: Winals y de Bassols, Carlota  APPLICANT: Watanabe, Yoshihiro  APPLICANT: Watanabe, Yoshihiro  APPLICANT: Watanabe, Yoshihiro  APPLICANT: Watanabe, Yoshihiro	Db 1440 AAACATGTGATCCTATAAGTTCCTTTTTCTAATCCTCAGGTTCCCTGA 1499  2529 TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGATATCATATTTGGAAATGC 2588  1500 TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGATATCATATTTTGGAAATGC 1559  Qy 2589 CTATTTAATACTTGTATTTTGCTTGACCCCTTTTGTAATGCATATTCATATTTTTTAATATTT 2648  1500 TATGATTCCTATACTTGTTTTTTTCATCCCCATTGAAGCCCATGAAGGCACTGTTTATTATATTTT 2648  1500 TATGATACTTGTATTTTTCATCCCCTTTTTGTTAAGGCACTGTTTATTATATTT 2648  1500 TATGATACTTGTTTTTTCATCTTTTTTCATTTGAATTCCCCCAGGAAGT 2708  1610 CTATTTAATACTTCTTTTTTCATCTTTTTCATCTAGATTCCCCCAGGAAGT 2708  Qy 2649 AATGCCATCATTATAGTGCTTTATCTTTTCATCTAGATTCCCCCAGGAAGT 1679  Qy 2709 GCCTAGAACATAATAGTGCTTTATCTTTCAACCCGGTTATTTTTCATCAAACCCTGATTCCT 1739  2709 GCCTAGAACATAATAGTGCTTATGCTTGACCCGGTTATTTTCAACCCCAGGAAACCTGATTCCT 1739  Qy 2769 TCTGTCCTGAACACATAAGCCAGGCAATTTTCCAACCCTTTTTTCAACTTGAGTTTGGTTATTTAAA 2828

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OY 1509 ACCACATTGGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAAAAAATAAT 1568	1449 AGAATATAAATGAGATAATCTAGCTTAA	1389 GAATGGTACATCTAGAGAACATTTGCCAAAGGCTAAGCACGGCAAAGGAAAATAAACAC	>->	QY 1269 TGCTACATATAATTAATTAATACCCTGACTAGGTTGGTGGAGGGTTATTACTTTTCAT 1328	QY 1209 AAATATGAAACTIGGTTGGGGAATCTCCCATTTTTCAATATTATTTTCTTCTTTGTTTTCT 1268	OY 1149 TITGGAAGACAGTATICAGAAAAAATTICCTTAATAAAAAAATACAACTCAGATCCTTC 1208	QY 1089 GTCAGTGATCABACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 1148	QY 1029 GATTCGACAGGGGATCCTTCGACTTTTCCATGTGGCCACACACA	Query Match 64.7%; Score 2028.4; DB 13; Length 2061; Best Local Similarity 99.8%; Pred. No. 0; Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;	; LENGTH: 2061 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-294-025-917	; CURRENT FILING DATE: 2002-11-12 ; NUMBER OF SEQ ID NOS: 1038 ; SOFTMARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 917		; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Stolk, John A. ; APPLICANT: Kalos, Michael D.	RESULT 11 US-10-294-025-917 i Sequence 917, Application US/10294025 i Publication No. US20030185830A1	2040 GTACTATTGTGTCAAG		Db 1920 GTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGCCAAACC 1979 Qy 3009 TCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAAGTGAAAAATAAA 3068
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 2034
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/966,459A
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,833
PRIOR APPLICATION NUMBER: 60/261,776
PRIOR APPLICATION NUMBER: 60/261,776
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/313,202
PRIOR APPLICATION NUMBER: 60/313,202
PRIOR FILING DATE: 2001-08-17
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Publication No. US20030022237A1
GENERAL INFORMATION:
APPLICANT: FEDER, J.N.
APPLICANT: HAWKEN, D.R.
APPLICANT: HAWKEN, D.R.
APPLICANT: CACACE, A.
APPLICANT: BARBER, L.
APPLICANT: KORNACKER, M.G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY4,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG
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Best Local Similarity
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                                                             ATTTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGT
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-916
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US-09-759-143-916
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Best Local Similarity
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TCACAGTTCAGCTTCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATAC
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: XL, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
112 TCACAGTTCAGCTTCATGATGGTGGAICCCAAIGGCAAIGAATCCAGTGCTACATAC
                                                                                                                            ACCTCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAAAAT 3065
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    TACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTAT
                     TACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGGAATCTCCATTTTTTCAATATTAT
                                                            GATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAATTTCCTTAAT-AAAAA
                                                                             GCTTCAGAGCCCTAGGTGTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCA
                                                                                                                                      GCTTCAGAGCCCTAGGTGTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCA
                                                                                                                                                                           GGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACAC
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LI, Samuel

LI, Samuel

APPLICANT: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION UNIVER: US/09/780,669

CURRENT APPLICATION NUMBER: US/09/780,669

CURRENT APPLICATION NUMBER: US/09/780,669

NUMBER OF SEQ ID NOS: 943

SOFTWARE: FALSEQ for Windows "

LENGTH: 1302

TYPE: DNA

ORGANISM: US-09-76
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Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
CTCATCTCCACCTCATCCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACC
                                                                              GAGCACAGCCTGCATGAGCCCATGTATATTTTCTTTGCATGCTTTCAGGCATTGACATC
                                                                                                                                                       TGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACT
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
                                                                                                                                                                                                    TTCATCCTAATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTG
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Mitcham, Jennifer L.
Harlocker, Susan L.
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Pred. No. 3.9e-303;
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1131	.072 GCTTCAGAGCCCTAGGTGTCAGTGATCAAACT
1071	1012 GGAGTGAAGACAAAGGAGATTCGACAGGGGATCCTTCGACTTTTCCATGTGGCCACACAC
1011	2 CCCGTCATCTTGGCCAATATCTATCTGCTGG
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771	712 ATCCGGGTCAAIGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCA
711	652 AATATCCTTTCCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGAT
651 600	92 GGGCTGCACTGATGGCACCCCTTCCTGTCT
591 540	532 CATGCCACAGTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGTGGTGCGG
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360	301 CTCATCTCCACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACC

Search completed: February 10, 2004, 02:26:47 Job time: 1064 secs

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## SUMMARIES

4384	Result No.
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# ALIGNMENTS

	COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE		OKOMET ON	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BX092732	RESTE. TO
RZPD Deutschee Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGp9981054063. RZPDLIB; I.M.A.G.E. CDNA Clone Collection; Human UnigeneSet - RZPD2 (RZPDLIB NO.972) http://www.rzpd.de/CloneCards/cgi- bin/showLib.pl.cgi/response7libNo-972 Contact: Ina Rolfs ERZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany	Contact: Ina Rolfs	Unpublished	Radelof, U., Schneider, D. and Korn, B. Human UnigeneSet - RZPD3	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,	1 (bases 1 to 702)	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	FIGURE GARLEGIA	HOHO RADIOTA	Homo sapiens (human)	EST.	BX092732.1 GI:27825459	BX092732	IMAGE:1602508, mRNA sequence.	BX092732 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGp998I054063 ;	BX092732 702 bp mRNA linear EST 23-JAN-2003		

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Fax: +49 30
www.rzpd.de
This clone i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free from RZPD; contact RZPD (cloneerzpd.de) for further information. Seq primer: M13r, Primer sequence: TTRCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                            GAGTIGGGTATTATAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCA 2870
                                                                                    TCATCAAACCTGATICCTTCTGTCCTGAACACATAGCCCAGGCAATTTTCCAGCCTTCTT
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//note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; list strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
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727; Conserv
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AU138663
AU138663.1
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HRI human cDNA project; 5'- & 3'-
Research Institute; cDNA library
Virology, Institute of Medical Sc
Helix Research Institute.
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AU138663
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1 (Dases 1 to 73)

Ota.T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1532-3 Yana, Kisarazu,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Takao Isogai
Genomics Laboratory
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TTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAA
                                                             TGCTACATATTAATTAATAACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT
                                                                                                                    AAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTTCTTTGTTTTTCT
                                                                                                                                                       TTTGGAAGACAGTATTCAGAAAAAAATTTCCTTAAT-AAAAATACAACTCAGATCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="placenta"
/clone lib="PLACE1"
/note="Vector: pME18SFL3"
145 c 122 g 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1009039"
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Pred. No. 2.9e
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ura,Y., Nagai,T., Su
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Sugano,S. and
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RESULT 3
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             Query Match
Best Local Similarity 98.
Matches 611, Conservative
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MEDLINE
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                                                                                                                                                                                                             Contact: Bepler G
Medicine and Radiology
Duke University Medical Center
Box 2610, MSRB, Room 117, Durham, NC 27710,
part of a 1.4 megabase contig including the
                                                                                                                                                                                                                                                                                   99134294
9933563
                                                                                                                                                                                                                                                                                                                          Bepler,G., O'Briant,K.C., Kim,Y.C., Schreiber,G. and Pitterle,D.M. A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOH11A metastasis suppressor
                                                                                                                                                                                            Suppressor region Class: unknown.
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 765)
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AF101565
AF101565.1 GI:4
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AF101565 Human Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="11p15.5"
/clone="pAc298E1177end"
/clone_lib="Human"
a 149 c 134 g 261
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                         19.3%;
98.9%;
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              0,
             Score 606.8; DB 28
Pred. No. 3.5e-54;
0; Mismatches 7;
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RESULT 4
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LOCUS
DEFINITION
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                ORGANISM
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1143 row: p column: 21
High quality sequence stop: 601.
High quality sequence stop: 601.
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BF679294
BF679294.1 GI:
EST.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/lab host="DH10B (T1 phage-resistant)"
/clone libb="NH10B (T1 phage-resistant)"
/clone libb="NH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: pDNR-LIB (Cl
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/mol_type="mRNA"
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Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMM 5 10 ---
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1 (Dases 1 to 779)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 572.
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Pred. No. 4.5e
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AI694767/c
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                                                                                                                                                                                                                                                                                                                                                          CDNA Library Proparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome (Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 661 Std Error: 0.00
Seq primer: -40UP from Gibco
   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 559)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI694767.1 GI:4982667
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                                                       /clone_lib="NCI_CGAP_Lu24" vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                          tissue_type="carcinoid"
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 17.4%;
98.4%;
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Score 544.6; DB 9;
Pred. No. 1.2e-47;
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sapiens cDNA clone IMAGE:2343810
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1 (bases 1 to 862)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                   Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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602137641F1 NIH_MGC_83 Homo
                                                                         http://image.llnl.gov
Plate: LLCM1090 row: b column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BF674130
                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                            Unpublished
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                                      Location/Qualifiers
organism="Homo sapiens"
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/db_xref="taxon:9666"
/clone="IMAGE:4273834"
/clone="IMAGE:4273834"
/lab_host="DH1D8 [T] phage-resistant)"
/clone lib="NIH MGC.83"
/c
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Pred. No. 3.8e-45;
0; Mismatches 11;
                                               505 bp mRNA linear EST 18-DEC-1999
Homo sapiens cDNA clone IMAGE:2342385 3',
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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EST.
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CTCATAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCT 146
                                                                                                                                                                                                                                                                              AAGTGCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGAT
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                                     CTCATAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCT
                                                                                  TAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGG
                                                                                                                       TAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGG
                                                                                                                                                                                                   TCCTTCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTAT 2824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:2342385"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 7.7e-43;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 483)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
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Gene Index
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/db_xref="taxon:9606"
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National Cancer Institute, Cancer Genome Anat
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al Similarity 98.6%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NCI (CGAP Coll pool 1 LLAM 2644-2653, 2871-2872 (INAGE CloneIDs 1057416-1061255, 1144584-1145351); Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6,791-806; CGAP GC4 TAG_TISSUB=GC4 TAG_TISSUB=GC4 TAG_TISSUB=GETT Cell
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Pred. No. 4.5e-40;
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Anatomy Project

Hara, A.

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                                                                          BB653241 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone C630016M16 5', mRNA sequence.
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                                                            BB653241
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Tissue Procurement: Chris Mc
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Seq primer: -40UP from Gibco
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="juvenile granulosa tumor"
//ab_host="PH108"
/clone_lib="NCI_CGAP_C017"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Chazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasak: D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
NS., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashiraki, V.
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Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
KONDO,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Hayashizaki,Y.
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adul
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                  'clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="hippocampus'
dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                             'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="C630016M16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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SOURCE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 448)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                AA988520
or84a03.s1 NCI_CGAP_Lu5
                                                                                                          Homo
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AA988520.1
                                 Unpublished
                                            Tumor Gene Index
                                                                                                                                                              mRNA sequence.
                                                                                                                   Homo sapiens (human)
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BB550795 445 k
7b59a0795 NCI_CGAP_Lu24 Homo
mRNA sequence.
BE550795
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-GGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 971 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 338.
Location/Qualifiers
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                                                                                       CCAAACCTCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAA
AAATAAAGTACTATTGTGTCAAG 3084
                                                                                                                                                                                                     GCTATGTGTTÄCACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAAACTGTGCAGAG
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//clome lib="NCI_CGAP_LU5"
//note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/db_xref="taxon:9606"
/clone="IMAGE:1602508"
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/lab_host="DH10B"
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CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
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Location/Qualifiers
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1 (bases 1 to 445)
1 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
Email: cgapbs-r@mail.nih.gov
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CAAACCTCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAA 3062
                                                                                                                                                     GGCTCATAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAG 2942
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llarity 100.0%; P
Conservative 0;
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db_xref="taxon:9606"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 539 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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1 (Dases 1 to 447)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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                                            ATTCCTTCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATT
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/note="organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2273422"
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Pred. No. 5.8e-37;
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0;	y Match 14.1%; Score 441; DB 10; Length 450; Local Similarity 100.0%; Pred. No. 7.3e-37; hes 441; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Ma Best Loc Matches
yith a green was con.	/lab host="DHIOB" //lab host="DHIOB" //clone_lib="NCI_CGAP_Lu24" //clone_lib="NCI_CGAP_Lu24" //clone_rogan: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker: Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "  144 a 83 c 98 g 125 t	BASE COUNT
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(CGAP),	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project Tumor Gene Index Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Mi.	TITLE JOURNAL COMMENT
tomi;	mKNA Sequence.  BF433082.1 GI:11445245  BF433082.1 GI:11445245  EST. Homo sapiens (human) (Homo sapiens Metazoa, Chordata, Craniata, Ve. Mammalia, Eutheria, Primates, Catarrhini, 1 1 (bases 1 to 450)	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE
OV-2000 06 3',		RESULT 15 BF433082/c LOCUS DEFINITION
	3063 AATAAAGTACTATTGTGTCAAG 3084 	Qy 3
AA 3062    AA 28	3003 CAAACCTCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAA 	Db Qy
GC 88	2943 CTATGTGTTACACAGAGATAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGC	Qy db
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CT 2882	2823 ATTAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCT	Db Qy

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## ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX107037	RESULT 1
Mitchell,S.C. and Saffran,D.C. G protein-coupled receptor up-regulated in prostate cancer and uses	Raitano, A.B., Afar, D.E., Jakobovits, A., Faris, M., Hubert, R.S.,	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX107037.1 GI:13922563	AX107037	Sequence 1 from Patent WO0125434.	AXI07037 3136 bp DNA linear PAT 30-APR-2001		

Db 541 GTACTTACGTTGCTGTGTCATCAAAATTGGTGGTGGTGGTGGTGGTGGTGGTGGA 600  Qy 601 CTGATGGCACCCTTCCTGTCTTCATCAAGCAGCTGCTCTTCTGCTGGTGCGGGGGGTGCA 600  Qy 601 CTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTT 660	421 GATGCTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG	OY  301 CTGCATGAGCCCATGTATATATTTTCTTTGCATGCTTTGAGGCATTGACATCCTCCC 360	QY 181 ATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCTCCCATTGTGCTCCCTC 240	OY 61 GGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCCTG	Query Match Query	AC37756.1 3922564" AVDPNGNES SEMYIFLCM LLAMAFDRY ILSHSYCLH SAQAKAFGT VYGVKTKE 99	thereof  JOURNAL Patent: WO 0125434-A 1 12-APR-2001;  VIOGENESYS, Inc. (US) Location/Qualifiers 1. 3136 /mol_type="genomic DNA" /db xref="taxon:9606"  CDS 133- 1086 /note="unnamed protein product"
1621 AAGAGTACATTTACCTACGTTAATGTAACACACACTGTTCTGAGAGTTTTCACAGCA 1 1681 TAIGGACCCTGTTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAA		QY 1381 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAA 1440  1381 TGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAA 1440  1381 TGAGATAAGAATGGTACATTTAGAAACTTTGCCAAAAGGCCTAAGCACGGCAAAGGCAAAAGAAA 1440  QY 1441 ATAACACAGAATATAATAAAATGAGATAATCTAGCTTAAAACTTACCTCTTCAG 1500	OY 1261 IGITITICITIGCTACATATAATTAATAACCCTGACTAGGTTGGAGGGTTAATA 1320    Db   1261 TGTTTCTTGCTACATATAATTAATACCCTGACTAGGTTGGAGGGTTATTA 1320    Db   1261 TGTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGAGGGTTATTA 1320    Oy   1321 CTTTTCATTTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTC 1380	1141 GTTAACATTTTGGAGGACACTATTCAGAAAAAATTTCCTTAATAAAAAATACAACTCA	1021 ACAAAGGAGTCGACAGCGCATCCTTCGACTTTCCATGTGGCCACACAGCGCTTCAGAG	841 AAGGCATTTGCCATGTGCATCTCTCATGTGTGCGCGGGGTGACTCTCATGTGCCATCTTC  901 ATTGGATTGTCCATGTGCATCGCTTTAGCAAGCGGGGTGACTCTCCGCTGCCCGTCATC  901 ATTGGATTGTCCATGTGCATCGCTTTAGCAAGCGGGGTGACTCTCCGCTGCCCGTCATC  901 ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGGGTGACTCTCCGCTGCCCGTCATC  901 ATTGGACTATCTGCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATCGAGTGAAG  961 TTGGCCAATATCTATCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATCGAGTGAAG  961 TTGGCCAATATCTATCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATCGAGTGAAG  961 TTGGCCAATATCTATCTGCTGGTTCCTCCTGTGCTCAACCCCAATTGTCTATCGAGTGAAG	0-0 0-0

Db 3:	2881 CTGGCTCATAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGA 2940
Qy 3	2821 TTATTAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATAC 2880
ם מם	2821 TTATTAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATAC 2880
Qy 2.	2761 TGATTCCTTCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTA 2820
ב ממ	2761 TGATTCCTTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTA 2820
Qy 1:	2701 AGCAAAGTGCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACC 2760
Db 1:	2701 AGCAAAGTGCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACC 2760
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BASE COUNT	CTCAGG
	2401 TTANTAGTTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCCAAATTAC 2460
FEATURES source	341 GCAATCTGACTTAGGCATGGGAATCAGGCATTTTTGCTTCTGAGGGGGCTATTACCAAGGG 2
JOURNAL	41
REFERENCE AUTHORS TITLE	2281 AGGACCATGCTTTATTTGGGGCTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAA 2340
ORGANISM	2221 TCTTGAAGATAACATTGGCCTTTTGAGTGGACTCGTAGCTGGAAAGTGAGGGAATCTTC 2280
KEYWORDS	1161 TTCTGATAGGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGG 2
ACCESSION VERSION	2161 TTCTGATAGGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGG 2220
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	2041 GCCAATTACCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTA 2100
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Patent: WO 02061087-A 433 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     CTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCCTCC
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            This clone (DKFZp313F0432) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                            Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                         Bloecker, H., Boecher, M., Mewes, H.W., Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens mRNA; cDNA
AL833127
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="313 (synonym: hlcc2). Vector pTriplEx2; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
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/db_xref="taxon:9606"
/clone="DXFZp313F0432"
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1902 GAGATTTCCAGAGTCTTACATTTTCTAGAGGAGGTATTTAATTTCTTCTCACTCA	1842 CATGCCCAATCTCATATGATGTGGAAGAACTGTTAGAGAGACCAACAGGGTAGTGGGTTA 1901	1782 TGGGGATCAGTGAATTAAATGGGGTCATACAAGTATAAAAAATTAAAAAAAA	1722 TTAATTAGGCAAAGATATTATTAGTACCCTCATTGTAGCCATGGGAAAATTGATGTTCAG 1781	1662 TCTGAGAGTTTTCACAGCATATGGACCCTGTTTTTCCTATTTAATTTTCTTATCAACCCT 1721	1602 TTGGAAGTAAAGCCTTGAAAAGAGTACATTTACCTACGTTAATGAAAGTTGACACACTGT 1661	1542 AAATGACTTCTACAGAGAAGAAATAATTTTTCCTCTGGACACTAGCACTTAAGGGGAAGA 1601	1482 ACTATAACTTCCTCTTCAGAACTCCCAACCACATTGGATCTCAGAAAAATGCTGTCTTCA 1541	1422 CTAAGCACGGCAAAGGAAATAAACACAGAATATAATAAATGAGATAATCTAGCTTAAA 1481	1362 CTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGC 1421	1302 IGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAAATCTAAACTGCTTCTA 1361	1242 TCAATATTATTTTCTTCTTTGTTTTCTTGCTACATATAATTAAT	1182 TAATAAAAATACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTT 1241	1122 CTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAAA	1062 GGCCACACACGCTTCAGAGCCCTAGGTGTCAGTGATCAAACTTCTTTTCCATTCAGAGTC 1121	1002 AATTGTCTATGGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGACTTTTCCATGT 1061	942 CICTCCGCTGCCCGTCAICTTGGCCAATATCTAICTGCTGGTTGCTCCTGTTGCTCAACCC 1001	882 CATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGA 941
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2982 TCTGAAAAACTGTGCAGAGCCAAACCTCTGTCATTTGCAACTCCCACTTGTATTTCTAC 3041 2982 TCTGAAAAACTGTGCAGAGCCACACCTCTGTCATTTGCACTCCCACTTGTATTTCTAC 3041 2939 TCTGAAAAACTGTGCAGAGCCAAACCTCTGTCATTTGCAACTCCCACTTGTATTTGTAC 2998 3042 GAGGCAGTTGGATAAGTGAAAAATAAAGTACTATTGTGTCAAGAAAAAAAA	2 CALLARA ISLANCI I GEORGE LA LEGIS I ACACADA LA ALCACCAGA CATA LEGIS CALLARA I CACCAGA CATA LA CACCAGA CACAGA CAC	19 6	OZ GCCTTCTTTGAGTTGGGTATTATTAAATTCTGGCCATTACTTCCAATGTGAGTGGAAGTG 59 GCCTTCTTTGAGTTGGGTATTATTAAATTCTAGCCATTACTTCCAATGTGAGTGGAAGTG 50 GCCTTCTTTGAGTTGGGTATTATTAAATTCTAGCCATTACTTCCAATGTGGAAGTG					TOTAL	ACCARGAACTICAAATTACAAATACTAAAACATIGTGATICATATATATIGTGGTAAGTTTCATT	CAGGGGCTATTACCAAGGGTTAATAGGTTTCATCTTCAACAGGATATGACAACAGTGTTA	GGACTITGAGACCAGGAAAGCAATCTGACTIAGGCATGGGAATCAGGCATTITGCTTCT	GGARAGTGAGGGATTTCAGGACCATGCTTTATTTGGGGCTTTGTGCAGTATGGAACAG 	GAAGTATGGAATGGCAGGTCTTGAAGATAGCATTGGCCTTTTGAGTGTGACTCGTAGCT	THAAAAGTICCATAGGTGATICTGATAGGCAGTGAGGTTAGGGAGCCACCAGTTATGATG	82 CCATTATIGAAGATTUTTATTCAGAAAGTCTGCATAGGGCTTATTAGTTTTTTTTT	22 IIAIIGICCIGGICCANIIGCANIIACCIGIGICIIGGAAGAAGIGAITTCIAGGIICA 79 TTATIGICCIGGICCAAITGCCAAITACCIGIGICTCIGGAAGAAGIGAITTCIAGGIICA	

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JOURNAL REFERENCE
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AUTHORS
TITLE
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SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JAN-2002) Genome Center, University of Washi Box 352145, Seattle, WA 98195, USA On Jan 11, 2002 this sequence version replaced gi:8072576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 175073)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175073)

Kiul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC105936 AC027367
AC105936.1 GI:LB129413
AC105936.1 GI:LB129413
HTGS_PHASE1, HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
HOMO sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC105936 175073 bp DNA Homo sapiens chromosome 3 clone RP11-27N2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator ET; 67% of reads
Chemistry: Dye-terminator ET; 67% of reads
Chemistry: Dye-terminator Big Dye; 33% of reads
Assembly program: Phrap; version (0.990319
Consensus quality: 169829 bases at least Q40
Consensus quality: 172659 bases at least Q20
Consensus quality: 172659 bases at least Q20
Consensus quality: 172890 bases at least Q20
Insert size: 185500; 10.7% error; agarose-fp
Insert size: 174273; sum-of-contigs
Quality coverage: 6.4x in Q20 bases; sum-of-contigs
Quality coverage: 6.8x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
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Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: University of Washington Genome Center Center Code: UWGC
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31135
31235
31235
51217
51317
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3748
14303
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19752
                3647: contig of 3647 bp in length
3747: gap of unknown length
14322: contig of 10555 bp in length
14402: gap of unknown length
1975: contig of 5349 bp in length
1985: gap of unknown length
31134: contig of 11283 bp in length
31234: gap of unknown length
51216: contig of 1982 bp in length
51316: gap of unknown length
61020: contig of 29713 bp in length
61020: contig of 2713 bp in length
61020: contig of 21492 bp in length
gap
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CTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCC 676
                                                                                                                                 TTGACCGCTATGTGGCCATCTGTCACCCACTGCCCATGCCACAGTACTTACGTTGCCTC
                                                                                                                                                                                                                     AGATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTT
                                                                               GTGTCACCAAAATTGGTGTGGCTGCTGGTGCGGGGGGGCTGCACTGATGGCACCCCTTC
                                                                                                                                                                                                                                                                                                          AAATGCTGGCCATCTTCTGGTTCAATTCCACTACCAGTCCAGTTTGATGCTTGTCTGCTAC
                                                                                                                                                                                                                                                                                                                                                  AAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTAC
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                                                                                                                                                                         TTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACAGTACTTACGTTGCCTC
                                                                                                                                                                                                                                                             AGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTT
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138345
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/note="assembly name:Contig18"
/ 35530 c 36557 g 51709 t
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138344: gap of unknown length
5 175073: contig of 36729 bp in
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3748. .14302
/note="assembly_name:Contigll"
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138345. .175073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="3"
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mol_type="genomic DNA"
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Pred. No. 0;
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174434

616 174254

174314 5 5 6 174374 436

376

174494

316

174554

256

174614

196

174674

136

2

2777 GAACACHAGCCAGCCAHTTTCCAGCCTTCTTGAGTTGGGTATTATTAAATTCTGGCC 2836 	g g		1697 CCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTAGTAGTACCCTCATTG 1756	. 84
CATAATAGIGCTTAIGCTIGACACCGGTTAITTTCATCAAACCTGATTCCTTCTGTCCT 277	p 5		1637 ACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGGACCCTGTTTTT 1696	Db 92
CICIO I CALCATIGACIGOTOTI GOTCATCATIGAATCCCCCAGCAAAGIGCCIAGA 271	B 6		1577 TGGACACTAGCACTTAAGGGGAAGATTGGAAGAGCCTTGAAAAGAGTACATTTACCT 1636 	Db Qy
TACTICTATTICCIGCIGGACTGTAAGCCARGAGGCACTGTTATTATTATATGAATGTCAT	? <b>&amp;</b> &		1517 GGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAGAATAATTTTTCCTC 1576 	dg VQ
COTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATTTGGAAATGCCTATTTAA 259	g gy		1457 ATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCAACCACCATT 1516	D Qy
0-0	dd YQ		1397 CATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACACAGAATATA 1456 	Db 49
17 TCARCAGGATATGACAACACTGTTAACCAAGAAACTCAAATTACAATACTAAAACATGT 2 	, B &		1337 GCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTA 1396	Db Qy
	Ag Ag	UI	1277 ATAATTATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCAT 1336	Qy db
97	Db Qy		1217 AACTGGTTGGGGAARCTCCARTTTTTCAARATATTATTTTCTTCTTTGTTTTCTTGCTACAT 1276	g 62
37 GGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGGAATCTTCAGGACCATGCTTTATT 22	р д Оу		1157 ACAGTATTCAGAAAAAAATTTCCTTAATAAAAAATACAACTCAGATCCTTCAAATATGA 1216 	당 성
77 GGTTAGGAGCACCACTTATGATGGGAAGTATGGAATGGCAGGTCTTGAAGATAACATT 22	4g 4g		1097 TCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTTAATGTTAACATTTTTGGAAG 1156	망양
17 AGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATAGGCAGTGA 217	) P &		1037 AGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAGGTGTCAGTGA 1096	dg VQ
57 TTGGAAGAAGTGATTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAAGTCTGCAT 211	g 28		977 TGCTGGTTCCTCTGTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGAC 1036	B &
97 TGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTACCTGTGTC 205	y dd y	••	917 TGCATCGCTTTAGCAAGCGGGGTGACTCTCGGCTGCCCGTTCATCTTGGCCAATATCTATC	B 8
37 ATTRAITECTECTCACTCAFCCAGTGTTGTATTRAGAAATTFCCTGGCAACAGAACTCA	D dg		857 GCGTCTCTCATGTGTGTGTGTGTGTTCATATTCTATGTACCTTTCATTGGATTGTCCATGG 916	B 6
77 GAGAGACCAACAGGTAGTGAGTTAGAGATTTCCAGAGTCTTACATTTTCTAGAGAGGTGTTAGATGAGGAGGTGTTAGATTTTCTAGAGGAGGTGTGAGAGTGTTAGATTTTCTAGAGGAGGTGGAGGTGTAGAGGAGGTCTTACATTTTCTAGAGGAGGAGGTGTAGAGGAGGTGTAGAGGAGGTGTAGAGGAG	, D &	-	797 TTATTCTTAAGACTGTGTGGGCTTGACACGTGAAGCCCAAGGCAATTTGGCACTT 856	B 8
TAAAAATTAAAAAAAAAAAAACATTCATGCCCAATCCCATAGGATGGAAGAACTGTTA 187	ם אף		737 TTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATATCTCCCATATCTGC 796	g &
TAGCCATGGGAAAATGATGTTCAGTGGGGATCAGTGAATTAAATGGGGTCATACAAGTA 18	, B &	<b>#</b>	677 TACACCAAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCC 736 	B 8
174 CCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTACCCTCATTG 173	<del>9</del>	, , , , , , , , , , , , , , , , , , ,		дb

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Erown, A., Camaratta, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazaree, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Weneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., North, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribe, R., Santos, R., Schauser, S., Schupback, R., Seaman, S., Severy, P., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Thodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                        Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 17917)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgelter, B.,
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Cooke, P., DeArellano, K., Dewar, K., Dizz, J.S., Dodge, S., Raro, S.,
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Hagos, B., Hotton, L., Hulme, W., Iliev, L., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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1 (bases 1 to 179177)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 11, clone RP11-648B16
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Homo sapiens chromosome 11, clone RP11-648B16, complete sequence.
                                                                                                                                                                                                                                                                                                                                                Submitted (09-MAR-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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            Lehoczky, J., Levine, R.,
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 11, 2002 this sequence version replaced gi:17402791. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 648_B_16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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/clone_lib="RPCI-11 Human Male
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complement(18070. .18306)
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2057 THEGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAAGTCTGCAT 2116	937 ATTTAATTTCTTCACTCATCCAGTGTTGTATTAGGAATTTCCTGGCAACAGAACTCA 1	1817 TAAAAATTAAAAAAAAAAAAAAGACTTCATGCCCAATCTCATATGATGTGGAAGAACTGTTA 1876	1697 CCTATITAATTITCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTACCCTCATTG 1756	1577 TGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGTACATTTACCT 1636.	1457 ATAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTCAGAACTCCCAACCACATT 1516	1337 GCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTA 1396	1217 AACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTTGTTTG	1037 AGGGCATCCTTCGACTTTTCCATGTGGCCACACGCTTCAGAGCCCTAGGTGTCAGTGA 1096
RESULT 6 AX201144 AX201144 2061 bp DNA linear PAT 29-AUG-2001 LCCUS AX201144 2061 bp DNA linear PAT 29-AUG-2001 DEFINITION Sequence 774 from Patent WO0151633.	QY 3017 TTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAAATAAGTACTATT 3076	53545 TCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACCTTGGGAAGCTATGTGTTACACA 5 2957 GAGTAAATCACCAGAAGCCTGGGATTTCTGAAAAAACTGTGCAGAGCCAAACCTCTGTCAT 3 [	53665 GAACACATAGCCAGCCAGTGAATTTCCAGCTTCTTTGAGTTGGGTATTATAATTCTGGCC 5  2837 ATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCCC 2  11111111111111111111111111111111	785 CTCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCAGCAAAGTGCCTAGAA 717 CATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCTTTCTGTCCT 717 CATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCTTTCTGTCCT 718 CATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAACCAGCATTATTCTGTCCT 725 CATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAACCAGATTATTAAATTCCTGTCCT 727 GAACACATAGCCAAATTTTCCAGCCAGCTTTTTTTGAGGTTGGGGTATTTAATTAA	53905 CCTATAACATGCTTCATCCCCTTTTGTAATGGATATCATCATTATTGAATGTCATCAT  2597 TACTTGTATTTGCTGCTGGACTGTTAAGCCCATGAGGGCACTGTTTATTATTGAATGTCAT  1	2417 TCAACL 54025 TCAACL 2477 GATCA'               53965 GATCA'	2297 TGGGGCTTTGTGCAGTATGGAACAGGACCTAGGAAGCCAGGAAGCAATCTGAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCCAGGAAGCAATCTGACTTAGGCTTTGAGACCAGGAAAGCAATCTGACTTAGGCTTCATAGAGACCAGGAATAAGGTTTCATCT 2357 ATGGGAATCAGGCATTTTTGCTTCTGAGGGGCTAATTACCAAGGGTTAATAAGGTTTCATCT [	2117 AGGGCTTATAGCAAGTTATTTATTTTAAAAGTTCCATAGGTGATTCTGATAGGCAGTGA 217  [

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689 CTGTTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTAGTAC 1748	1688	569 TTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGTAC 1628	509 ACCACATTGGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAGAAATAAT 1568   C	449 AGRATATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA 1508	389 GAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACAC 1448	329 TITACCATGCAGICCAAATCIAAACIGCTTCTACTGATGGTTTACAGCATTCTGAGATAA 1388	269 TGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT 1328	209 AAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTCT 1268	149 TTTGGAAGACAGTATTCAGAAAAAAATTTCCTTAATAAAAATACAACTCAGATCCTTC 1208	1089 GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 1148	GGCCACACACGCTTCAGAGCCCTAGGT 1088	cch 1 Similarity 99.8%; Pred. No. 0; 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;	/mol_type="genomic DNA" /db_xref="taxon:9606" 612 a 383 c 399 g 667 t	e 1. 2061 e /organism="Homo sapiens"	<pre>vang, A. and Meagher, M.J. for the therapy and diagnosis of prostate l9-JUL-2001;</pre>	on,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates: Catarrhini; Hominidae, Homo	AX201144 AX201144.1 GI:15390908
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2769 TCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATTAAA	2709 GCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCT	2649 AATGTCATCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCCAGCAAAGT	56.0	00	0 4	80	2349 ACTTAGGCATGGGAATCAGGCATTTTTGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG	60	00		2109 GTCTGCATAGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA		1989 AGAACTCATGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTA	1929 GAGGAGGTAITTAAITTYCTTCICACTCATCCAGTGTTGTATTTAGGAATTTYCCTGGCAAC 	40	82 4	4 4 6	

8 8 8 8 8	Ag ag	Best Loc Matches Qy 1	BASE COUNT ORIGIN	FEATURES sourc	TITLE JOURNAL	REFERENCE AUTHORS	SOURCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 7 AX267943	A 4	A 48	da Yo	g Q	Qy db
1149 ITTGGAAGACAGTATTCAGAAAAAATTCCTTAATAAAAATACAAGTCAGATCCTTC 1208	GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 1 	al Similarity 99.8%; Pred. No. 0; 2052; Conservative 0; Mismatches 1; Indels 3; 029 GATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAGC	/mol_type="geno" /db_xref="taxon 612 a _383 c _39 tch _64.7%; So	CORIXA CORPORATION (US) Location/Qualifiers 1. 2061 ce /organism="Homo sapiens	and Henderson,R.A.  Compositions and methods for the therapy and diagnosis of prostate cancer  Patent: WO 0173032-A 917 04-OCT-2001:	1, Dillon,D.C., Mitcham,J.L., Harlocker,S.L., J. Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., D. Vedvick,T.S., Carter,D., Li,S.X., Wand,A., Skeik,v. V.	Homo sapiens (buman) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	ON Sequence 917 from Patent WO0173032.  N AX267943 AX267943.1 GI:16516537	NAT1043 2001 15 14 14 14 14 14 14 14 14 14 14 14 14 14	3069 GTACTATTGTGTCAAG 3084 	3009 TCTGTCATTTGCAACTCCCACTTGTATTTGTACGAGGCAGTTGGATAAGTGAAAAATAAA 3068 	2949 GTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGCCAAACC 3008	2889 TARARCCCTCCCATGTGCAGCCTTTCATGTTGACATTARATGTGACTTGGGARGCTATGT 2948	2829 TICTGGCCATTACTICCAATGTGAGTGGAAGTGACATGTGCAATTICTATACCTGGCTCA 2888 
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1200 ATAACATTGGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGGAATCTTCAGGACCAT 2289 GCTTTATTTGGGGCTTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAAGCAATCTG 1260 GCTTTATTTGGGGCTTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAAGCAATCTG 1260 GCTTTATTTGGGGCTTTGTGCAGTATGGAACAAGGACTTTGAGACCAGGAAAGCAATCTG 2349 ACTTAGGCATTGAGGAATTATGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG 11111111111111111111111111	2169 1140 2229	10 21 10	19 9 20	19	1869		1749 722							

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  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
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Query Match
Best Local Similarity
Matches 2052; Conserv
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Primer for synthesizing full-length cDNA and use thereof FH F
Location/Qualifiers
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PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
CCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGGGTCA
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-	2888 1859	2829 TTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGGCTCA	
	2828 1799	2769 TCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATAAA	
	2768 1739	2709 GCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCT	
	2708 1679	2649 AATGTCATCGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCCAGCAAAGT	
	2648 1619	2589 CTATTIAATACTIGTATITGCIGGACTGTAAGCCCAIGAGGGCACTGTTTATTATIG	
	2588 1559	2529 TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATTTGGAAATGC	
	2528 1499	2469 AAACATGTGATCATATATGTGGTAAGTTTCATTTTCTTTTTCAATCCTCAGGTTCCCTGA	
	2468 1439	2409 TITCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTACAAATACTA 	
	2408 1379	2349 ACTTAGGCATGGGAATCAGGCATTTTTGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG	
	2348 1319	2289 GCTTTATTTGGGGCTTTGTGCAGTATGGAAACCAGGGACTTTGAGACCAGGAAAGCAATCTG	
	2288 1259	2229 ATAACATTGGCCTTTTGAGTGTGACTCGTAGCTGGAAAGTGAGGGAATCTTCAGGACCAT	
	2228 1199	2169 GGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGGAATGGCAGGTCTTGAAG	
	2168 1139	2109 GTCTGCATAGGGCTTATAGCAAGTTATTTATTAAAAGTTCCATAGGTGATTCTGATA	
	2108 1079	2049 CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA	
	2048	1989 AGAACTCATGGCITTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTA	
	1988 959	1929 GAGGAGGTATTTAATTTCTTCTCACTCATCCAGTGTTGTATTTAGGAATTTCCTGGCAAC	
	1928	1869 AACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTA	
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Best Local Similarity 99.8
Matches 2052; Conservative
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CE (bases 1 to 2061)

CE (bases 1 to 2061)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1522-3 Yana, Kisarazu, Chiba 292-0812, Japan Submitted (23-AUG-2000) Takao Isogai, Helix Research Missitute, Genomics Laboratory; 1522-3 Yana, Kisarazu, Chiba 292-0812, Japan Genomics Laboratory; 1522-3 Y
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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     GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT
                                                                                                GATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAGCCCCTAGGT
                                                                GATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAGGT
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/mol_type="mcNA"
/db_xref="taxon:9806"
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/tissue_type="placenta"
/clone_Tib="PLACE1"
/clone="cloning vector: pME18SFL3"
2 a 383 c 399 g 667 t
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ACO25249  ACO25249  Homo sapiens chromosome 11 clone RP11-648B16, WORKING DRAFT SEQUENCE, 8 unordered pieces.  ACO25249  ACO25249  ACO25249  ACO25249:  AC	069 GTACTA        040 GTACTA	1920 GTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGCCAGAACC 3008 1920 GTTACACAGAGTAAATCACCAGAAGCCTGGATTTCTGAAAAAACTGTGCAGAGCCAAACC 1979 1920 GTTACACAGAGTAAATCACCAGCTGGATTTCTGAGTGAAAAACTGTGAAAAACTAAA 3068 1900 TCTGTCATTTGCAACTCCCACTTGTATTTTGTACGGCCAGTTGGATAAGTGAAAAATAAA 2039	889 TAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCTATGT	2829 TTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGGCTCA 2888 	2769 TCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATTAAA 2828 	09 GCCTAGAACATAATAGTGCTTATGCTTGACACCGGTTATTTTTCATCAAACCTGATTCCT 	2649 AATGTCATCTCTGTTCATCATTGACTGCTCTTTGCTCATCATTGAATCCCCCAGCAAAGT 2708 	2589 CTATTTAATACTTGTATTTGCTGCTGGACTGTAAGCCCATGAGGGCACTGTTTATTATTG 2648	2529 TATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGATATCATATTTGGAAATGC 2588 	2469 AAACATGTGATCATATATGTGGTAAGTTTCATTTTCTTTTTCAATCCTCAGGTTCCCTGA 2528	2409 TTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAAACTCAAATTACAAATACTA 2468 	2349 ACTTAGGCATGGGAATCAGGCATTITTGCTTCTGAGGGGCTATTACCAAGGGTTAATAGG 2408	2289 GCTTTATTTGGGGCTTTGTGCAGTATGGAACAGGGACTTTGAGACCAGGAAAGCAATCTG 2348	ATAACA

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Chemistry: Dye-primer ET; 92% of reads
Chemistry: Dye-terminator Big Dye; 8% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 176953 bases at least Q30
Consensus quality: 178421 bases at least Q30
Consensus quality: 178421 bases at least Q30
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Submitted (07-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63188, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 180000; agarose-fp
Insert size: 178964; sum-of-contigs
Quality coverage: 5.37 in Q20 bases; agarose-fp
Quality coverage: 5.41 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 179664)
Waterston, R.H.
The sequence of Homo sapiens clone
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Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it be preserved.
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26007
                                        /note="assembly_name:Contig5"
141217. .145469
                                                                                                                          /note="assembly_name:Contig11'
63532. .136359
                                                                                                                                                              /note="assembly_name:Contig10" 26007. .63431
  /note="assembly_name:Contig6'
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                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="genomic DNA"
                                                                                                                                                                                                                          clone="RP11-648B16"
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145469; contig of 4253 bp in length
145569; gap of unknown length
154743: contig of 9174 bp in length
154843: gap of unknown length
165973: contig of 11130 bp in length
166073: gap of unknown length
179664: contig of 13591 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25906: contig of 25906 bp in length 26006: gap of unknown length 63431: contig of 37425 bp in length
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                                                                                                                                                                                                                                                                                                                                              'Qualifiers
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TCCAGTGTTGTATTTAGGAATTTCCTGGCAACAGAACTCATGGCTTTAATCCCACTAGCT 2016
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                                                                                                                     GACTTCATGCCCAATCTCATATGATGTGGAAGAACTGTTAGAGAGACCAACAGGGTAGTG
                                                                                                                                                          GACTTCATGCCCAATCTCATATGATGTGGAAGAACTGTTAGAGAGACCAACAGGGTAGTG 1896
                                                                                                                                                                                                TTCAGTGGGGATCAGTGAATTAAATGGGGTCATACAAGTATAAAAATT--AAAAAAAAA
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                                                                             CTTCAAAATGACTTCTACAGAGAAGAAATAATTTTTCCTCTGGACACTAGCACTTAAGGG
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Oy 592 GGGCTGCACTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCC 6	3037 TGTACGAGGCAGTTGGATAAGTGAAAAATAAAGTACTATTGTGTCAAGAAAAAAAA	S
32 CATGCCACAGTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGGTGGTGCTGCGGGTGCTGCTGCTGC	2977 GGATTICTGAAAAAACTGTGCAGAGCCAAACCTCTGTCATTTGCAACTCCCACTTGTATT 3036	D Qy
472 TCCACAGTGCTGCCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCACTGCGC	2917 GTTGACATTAAATGTGACTTGGGAAGCTATGTGTTACACAGAGTAAATCACCAGAAGCCT 2976	Db Qy
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OY 292 GAGCACAGCCTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATC: 3	2737 ACACCGGTTATTTTCATCABACCTGATTCCTTCTGTCCTGAACACATAGCCAGGCAATT 2796	P 62
OY 232 TGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACATCATCATCATCTACATTGTGCGGACT 2	2677 TCTTTGCTCATCATTGAATCCCCCAGCAAAGTGCCTAGAACATAATAGTGCTTATGCTTG 2736	ру
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J 2	2497 TCATTTTCTATTCTATCCTCAGGTTCCCTGATATGGATTCCTATAACATGCTTTCATCC 2556	dg Vg
Query Match Best Local & Matches 1300	2437 TGTTAACCAAGAAACTCAAATTACAAATACTAAAACATGTGATCATATATGTGGTAAGTT 2496 	g gg
VT 277 a 346 c 259 g 420 t	2377 CTTCTGAGGGGCTATTACCAAGGGTTAATAGGTTTCATCTTCAACAGGATATGACAACAG 2436	dg Vy
source 1. 1302 /organism="Homo sapiens" /mol_type="genomic DNA"	2317 AACAGGGACTTTGAGACCAGGAAAGCAATCTGACTTAGGCATGGGAATCAGGCATTTTTG_2376	9 8
	83 1	₽ \$
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Mang,A. and Meagher,M.J. Compositions and methods for the therapy and disgnosis of prost.	197 TGATGGGAAGTATGGAATGGCAGGTCTTGAAGATAACATTGGCCTTTTGAGTGTGACTCG 225	S B 8
	2137 TATTTTTAAAAGTTCCATAGGTGATTACGGATAGGCAGTGAGGTTAGGGAGCCACCAGTTA 2196	B &
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Mismatches 2; Indels 1;
                                                                                             TITGACCGCTAIGTGGCCAICTGTCACCCACTGCGC
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ager,G.R., Day,C.H., Retter,M.W.,
fang,A. and Meagher,M.J.
for the therapy and diagnosis of prostate
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es; Catarrhini; Hominidae; Homo.
CTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCC 651
                                                        AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACC
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SOURCE Homo sapiens (human)  ORGANISM Homo sapiens (human)  NORGANISM Homo sapiens  Eukaryota, Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi;  Eukaryota, Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi;  REFERENCE 1  AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,  Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.; Hepler,W.T.  and Henderson,R.A.  Compositions and methods for the therapy and diagnosis of prostate cancer  JOURNAL Patent: WO 0173032-A 916 04-OCT-2001;  FEATURES Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  /organism="Homo sapiens"	RESULT 12 AX267942 LOCUS AX267942 AX267942 AX267942 AX267942 AX267942 AX267942 AX267942 AX267942 AX267942 AX267943 ACCESSION AX267942 VERSION AX267942.1 GI:16516536 KEYMORDS	1252 TTTCTTCTTTGTTTTCTTGCTACATATAATTAATAACCCTGAC	Qy 1132 GATTITAATGITAACATTITGGAAGACAGTAITCAGAAAAAAATITCCTTAATAAAAAA 1191	Qy 1012 GGAGTGAAGACAAAGGAGATTTGACAGCTTTTCCATGTGGCCACACAC 1071	Qy  892 GTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTG 951	Qy 772 CTTCTCATCTCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGCACACGTGAA 831	Qy 652 AATATCCTTTCCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGAT 711 Db 601 AATATCCTTTCCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGAT 660  Qy 712 ATCCGGGTCAATGTCGTCTATGGCCTTATCGTCATCATCATCTCCGCCATTGGCCTGGACTCA 771
OY  772 CTTCTCATCTCCTTCTCATATCTGCTTAAGACTGTGTTGGGCTTGACACGTGAA 831  Db 721 CTTCTCATCTCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAA 780  721 CTTCTCATCTCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACGTGAA 780  OY  832 GCCCAGGCCAAGGCATTTGGCACTTGCGTCTCCATGTGTGTG	Qy 652 AATATCCTTTCCCATTCCTACTGCCTACAGCAGATGTCATGAAGCTGCCCTTCTGCGCTCC 600  Qy 652 AATATCCTTTCCCATTCCTACTGCCTACAGCAAGATGTCATGAAGCTGGCCTGTGATGAT 711	532 CATGCCACAGTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGTGGTGCGGGGGGGG	Qy 412 ATCCAGTTTGATGCTTGCTGCTACAGATTTTTTGCCATCCACTCCTTATCTGGCATGGAA 471	Qy 292 GAGCACAGCCTGCATGAGACCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATC 351	QY 172 TICATICCTAATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTG 231	Qy  52 TGGACAAGGGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCCTG	/mol_type="genomic DNA"  Ab_xref="taxon:9606"  BASE COUNT 277 a 346 c 259 g 420 t  ORIGIN  Query Match Best Local Similarity 99.8%; Pred. No. 2.1e-274; Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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REMARK
COMMENT
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TITLE
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                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: n Column: 16.
                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens, clone MGC:24137 IMAGE:4694856, mRNA, BC0222401 GI:18490239 MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Submitted (01-FEB-2002) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/translation="MVDPNGNESSATYFILIGLEGLEEAQFWLAFFLCSLYLIAVIGN
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Query Ma Best Loc Matches Qy	atch 37.8%; Score 1186.4; DB 9; Length 1225; cal Similarity 99.5%; Pred. No. 6e-252; 1190; Conservative 0; Mismatches 6; Indels 0; Gaps 0; 1 CAGAGAGGCTGTATTTCAGTGCAGCCTGCCAGACCTTCTTGGAAGAACACTGGACAAAG 60
φ <b>γ</b>	1 GGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCCTG
D 43	6 GGGGTCACACATTCCTTCCATA
Ş	TTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCA
₽ B	136 AGCTTCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTA 195
8	GGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCC
Дb	196 ATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTC 255
8	ACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGA
Db	256 TACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGC 315
γŞ	ATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATC
дъ	316 CTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCC 375
Ϋ́	CATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAG
Вb	CICATO
Ş	421 GATGCTTGTCTGCTACAGATTTTTGCCATCCATCCTTATCTGGCATGGAATCCACAGTG 480
מם	436 GATGCTTGTCTGCTACAGATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG 495
δ	GCTATGTGGCCATCTGTCACCCACTGCGCCATGCCAC
Db	CATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACA 5
\$	TACTTACGTTGCCTCGTGTCAC
Db	CTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGGTGCGGGGGGCT
. VQ	ACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATAT
Db	616 CTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTT 675
Ϋ́	CATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGATATG
Dβ	
Ş	GTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCAT
DЬ	736 AATGTCGTCTATGGCCTTATCGTCATCATCTCGCCATTGGCCTGGACTCACTTCTCATC 795
VΩ	CTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGG
В	796 TCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGGCTTGACACGTGAAGCCCAGGCC 855
ΥQ	41 AAGGCATTTGGCACTTGCGTCTCTCATGTGTGTGTGTGTG
Db	856 AAGGCATTIGGCACTIGCGTCTCATGTGTGTGTGTTCATATCTATGTACCTTTC 915

Quer Best Qy Qy Qy Db	BASE CO	FEATURE SO	ABFERENCE AUTHORS TITLE JOURNAL	AX64653 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db Db	Q
Query Match  37.8%; Score 1186.2; DB 6; Length 1354;  Best Local Similarity 99.3%; Pred. No. 6.6e-252;  Matches 1202; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  77 TCCATACGGTTGAGCCTCTACCTGCTGGTGCTGGTCACAGTTCAGCTTCTTCATGATGG 136  145 TCTTTGCATTCCAGCCTCTACCTGCTGGTGCTCACAGTTCAGCTTCTTCATGATGG 204  137 TGGATCCCAATGGCAATGAATCCAGTGCTACATCTCATCCTAATAGGCCTCCCTGGTT 196  119 TGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCCCTGGTT 264  197 TAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCAATGGTCCTCATGTGTC 256	/note="unnamed protein product" /codon_start=1 /protein_id="CAD69403.1" /db_xref="GI:28798937" /translation="MVDPNGNESSATYFILIGLEGLEEAQFWLAFPLCSLYLIAVLGN /translation="MVDPNGNESSATYFILIGLEEAQFWLAFPLCSLYLIAVLGN /TIIYIVRTEHSLHEPMYIFICMLSGIDILISTSSMPXMLAIFWFNSTTIQFDACLLQ MFA.HISLSGNESTVLIAMAFDRYVAAICHPLAHATVLTLPRVTXIGVAAVVEGAALMAP LPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISF SYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVFFIGLSMVHRFSKRRDSPLFVI LANIYLLVEPVLNFIVYGVKTKEIRQRILRLFHVATHASEP" COUNT 297 a 338 c 278 g 441 t	Source 1. 1354  source 1. 1354  /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"  201. 1154	Suwa,M., Asai,K., Akiyama,Y. & Suwa,M., Asai,K., Akiyama,Y. & Guanosine triphosphate-binding Patent: EP 1270724-A 745 02-JJ National Institute of Advanced Sci (JP) ; Center for Advanced Sci (JP)	SULT 14 646553 AX646553 AX646553 FINITION Sequence 745 from Patent EP1270724. CESSION AX646553 AX646553 RSION AX646553.1 GI:28798936 YWORDS URCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		901 ATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGGGTGACTCTCCGCTGCCCGTCATC
B & B & B & B & B	) B & B & B & B	QY QY	5 & & &	D	0 40 Qy	B & B & B & B
1097 TCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGTTTTAACATTTTTGAACA 1156	917 TGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCCAATATCTATC	865 TATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTTGGCACTT 924 857 GCGTCTCTCAIGTGTGTGTGTGTTCTATTTCTATGTACCTTTCATTGGATTGTCCATGG 916	THATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGC THILLIAN CONTROL OF THATCGTCATCATCTCCATCTCATATCTGC TTATCGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCATCTTCTCATATCTGC TTATTCTTAAGACTGTGTTGGCCTTGACACGTGAAGCCCACGGCCAAGGCATTTGGCACTT	557 GIGTOACCAAAATTGGIGTGGCTGCTGTGGTGGGGGGGGGGGCTCCACTGATGGCACCCCTTC 616	437 AGATTTTTGCCATCCATCCTTATCTGGCATGGAATCCACAGTGCTGGCCATGGCTT 496	265 TAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCCCTCTACCTTATTGCTGTGC 324 257 TAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCATGT 316

, Oy	B &	94 VQ	Query Match Best Local S Matches 1202	BASE COUNT ORIGIN			CDS	800.5	FEATURES		COMMENT	JOURNAL	JOURNAL REFERENCE AUTHORS TITLE	AUTHORS	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	AB065787 LOCUS DEFINITION	RESULT 15
197 TAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCTGTGC 256	137 TGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCCCTGGTT 196 	77 TCCATACGGTTGAGCCTCTACCTGCCTGGTGCTGGTCACAGTTCAGCTTCTTCATGATGG 136	/ Match Local Similarity 99.3%; Pred. No. 6.6e-252; les 1202; Conservative 0; Mismatches 8; Indels 1; Gaps 1;	SYLLILKTVLGITREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVI LANIYLLVPPVLNPIVYGVKTKBIRQRILKLFHVATHASEP" 297 a 338 c 278 g 441 t	/translation="MVDDINGNESSATYFILIGLEGLEEAQFWLAFFLCSLYLIAVLGN LTIIYIVRTEHSLHEPMYIFLCMLSGIDILISTSSMPKYLAIFWFWSTTLOFDACLLQ MFAIHSLSGMESTVLLAMAFDRYVAICHFILIAFRVTKIGVAAVVRGAALMAP LFVFIKQLFFCRSNILSHSYCLHQDVMKLACDDIAVAVVGLIVIIGAAIGLDSLLISF	<pre>/evidence=not_experimental /product="seven transmembrane helix receptor" /protein_id="BAC06006.1" /db xref="GI:31928840"</pre>	<pre>/db xref="taxon:9606" /chromosome="11" 2011154 /codon start=1</pre>		of Advanced Industrial Science and Technology (AIST)] and [Genom Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].  Location/Qualifiers	<pre>inding(GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction. And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute</pre>	Tel:81-3-3599-8080, Fax:81-3-3599-8081) This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene	Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/	Unpublished 2 (bases 1 to 1354) Suwa, M. Direct Submission	Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S., Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y. Genome-wide discovery and analysis of human seven transmembrane helix receptor genes			AB065787  Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_350.	
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1277 ATAATTATTAA 1287 	1217 AACTGGTTGGGGAATCTCCATTTTTCAATATTATTTTCTTCTTTGTTTTCTTGCTACAT 1276	1157 ACHSTATTCHSHAMANAATTTCCTTHATAARAANACHCAGACTCAGATCCTTCAAATAIGA 1216 	97 TCABACTTCTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTTAACATTTTGGAAG		977 TGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGAC 1036	917 TGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCCAATATCTATC	857 GCGICTCTCATGTGTGTGTGTGTCATATTCTATGTACCTTTCATTGGATTGTCCATGG 916	797 TTATTCTTAAGACTGTGTTGGGCTTGACACGTGAAGCCCAAGGCAAGGCATTTGGCACTT 856	737 TTATICGTCATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGC 796	677 TACACCAAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCC 736	617 CTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCC 676	557 GTGTCACCAAAATTGGTGTGGCTGCTGTGGTGGGGGGGGG	497 TTGACCGCTAIGTGGCCATCTGTCACCCACTGCGCCATGCCCACAGTACTTACGTTGCCTC 556	437 AGATTTTTGCCATCCATTCTTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTT 496	377 AAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTAC 436	317 ATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCCATGCCCA 376	257 TAGGTAACTTGACAATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCATGT 316	265 TAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACTTATTGCTGTGC 324

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Search completed: February 9, 2004, 19:19:58 Job time : 11169 secs

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## ALIGNMENTS

Human G-protein coupled receptor, PHOR-1. AAB85002; AAB85002 standard; Protein; 06-AUG-2001 (first entry) 317 AA.

G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine; cervical; stomach; rectal; cytostatic; vaccine; cell function regulator human; prostate homologue of olfactory receptor-1. regulator;

sapiens.

WO200125434-A1

05-OCT-2000; 2000WO-US27543

05-OCT-1999; 99US-0157902

(UROG-) UROGENESYS INC.

Raitano AB, Mitchell SC, Afar DEH, U Saffran DC; Jakobovits ۶ Faris Z Hubert

WPI; 2001-367230/38. N-PSDB; AAF83880.

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                 cancer-associated protein #87.
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Pred. No. 2.8e-169;
; Mismatches 0;
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                                                                                                                                                                                                                                                                       tissue; human; mammal;
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Best Local
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16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
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08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer as well as for useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting a prostate cancer-associated transcript in a cell in patient, useful for diagnosing prostate cancer (PC) or screenimedulators of PC, by determining if prostate cancer-associated are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-associated transcript in a cell fr comprises contacting a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 373; 436pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG61800-ABG61944 represent prostate cancer-associated proteins
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DB; ABK92202.
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RORILRLFHVATHASEP 317
                                                                                                                  CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
                                                                                                                                                                               AFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSY
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                                TCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI
                                                         TCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI
                                                                                                                                                         AFDRYVAICHPLRHATVLTLPRVTKIGVÄAVVRGAALMAPLPVFIKQLPFCRSNILSHSY
                                                                                           CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
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; 2001US-281922P.
; 2001US-286214P.
; 2001US-0847046.
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2000US-0733288.
2000US-0733742.
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2001US-276791P.
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Pred. No. 5.9e-169;
1; Mismatches 0;
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06-OCT-1998;
11-MAY-1999;
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Guegler
                            WPI; 2000-328934/28.
N-PSDB; AAA09351.
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                                                                                                                                                                                            06-OCT-1999;
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  human G-protein
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98US-0172211.
99US-0133585.
                                                                                                             PHARM INC.
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57
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272
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113..1;
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27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
                                                                                                                                                                             Homo
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                                                                                             27-MAR-2001;
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                                                                                                                                                   WO200173032-A2
                                                                                                                                                                                                       Human; prostate
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 2000US-0536857.
2000US-0568100.
2000US-0570737.
2000US-0593793.
2000US-0605783.
2000US-0636215.
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The GCRP polypeptides, polynuclectides, antibodies, antagonists ar agonists may be administered to human patients for the diagnosis, treatment and prevention of nervous system disorders (e.g. epileps stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory disorders, complications of cancer, hemadialysis and extracorporeal circulation, and cell proliferative disorders. The also used to treat or prevent disorders associated with decreased increased expression or activity of GCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes human G-protein coupled receptor protein (GCRP) The GCRP polypeptides, polynucleotides, antibodies, antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment and prevention of nervous system disorders, autoimmune/inflammatory disorders, and cell proliferative
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2001WO-US09919
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                                                                                                                                                                               immunostimulant; tumour; immunogen.
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5.9e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2000;
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r MW, Stolk (
Skeiky YAW, I
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318
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Pred. No. 5.9e-169;
1; Mismatches 0;
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; ancrexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; infection; human immunodeficiency virus; HIV.

WO200174904-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10241.

31-MAR-2000; 2000US-193664P, 06-APR-2000; 2000US-195065P, 06-APR-2000; 2000US-195066P, 06-APR-2000; 2000US-195066P, 06-APR-2000; 2000US-19506P, 06-APR-2000; 200US-19506P, 06-APR-2000; 200US-19506P, 06-APR-2000; 200US-19506P, 06-APR-2000;
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(CURA-) CURAGEN CORP.

Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna S Padigaru M, Mishnu VS, Tchernev VT, Spytek KA, Li L; Baumgartner JC, Gusev VY;

WPI; 2001-639351/73. N-PSDB; ABA81542.

New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and agonists useful therapeutically

Claim 1; Page 55; 157pp; English

The invention relates to nucleic acid sequences (ABA81529-ABA81522) that CC encode G-coupled protein-receptor related polypeptides
CC (ABB44523-ABB44543). The isolated polypeptide having a sequence differing
CC by no more than 15 % of amino acid residues from one of 22 amino acid
CC sequences (or mature forms of the sequences) fully defined in the
CC sequences (or mature forms of the sequences) fully defined in the
CC entiated in and corresponding to human G-protein coupled receptor x
CC (GPCRX) polypeptides. The polypeptides have potential cardiant,
CC entiated rissclerotic, anabolic, cytostatic and antiviral activity. The
CC polypeptides can be administered therapeutically, especially using gene
CC therapy and expressing the encoding DNA in vivo, to treat or prevent
CC GPCRX-associated disorders, especially in humans. For example, they can
be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
CC related to signal processing and metabolic pathway modulation (e.g.
CC obesity, amorexia), diabetes, osteoporosis, Crohm's disease, multiple
CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
CC disease, parkingon's disorder, Huntington's disease, multiple colleges, parkingon's disorders, developmental diseases, neurological disorders,
CC haematopoietic disorders, developmental diseases, neurological disorders,
CC mamunodeficiency virus (HTV)-1 or HTV-2). They can be used diagnostically
CC with altered levels of the polypeptide expression levels relative to

RESULT 5
ABB44533
ID ABB4
XX
AC ABB4
XX
DT 28-J
XX
DE Huma

ABB44533 standard;

Protein; 318

ABB44533;
28-JAN-2002
Human GPCR7a

(first entry)
polypeptide SEQ ID

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RESULT 6
AAUZ451
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Best Local S
Matches 316
                                                                                                                                                                   13-MAR-2000; 2000US-0188914.
24-MAR-2000; 2000US-0192033.
12-APR-2000; 2000US-0198474.
24-APR-2000; 2000US-029735.
26-MAY-2000; 2000US-0207702.
23-UNN-2000; 2000US-021849.
16-AUG-2000; 2000US-023684.
07-SEP-2000; 2000US-023684.
07-SEP-2000; 2000US-0236862.
WPI; 2001-570867/64
N-PSDB; AAS42254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human olfactory G protein-coupled receptuseful for screening for compounds involved in olfactory sensat where the compounds can be used in the food, pharmaceutical and
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Pred. No. 5.9e-169;
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Kalos MD,
 Human; G protein-coupled receptor; GPCR;
neuroleptic; nootropic; neuroprotective;
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99.7%;
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Pred. No. 5.9e-169;
1; Mismatches 0;
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Retter MW, Stolk JA,
CON198 protein; schizophrenia;
bipolar disease; psychotropic;
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neurological disorder; psychiatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease depression; migraine; genetic screening; chromosome 11.
WO200131014-A2
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                                                                                                                                                                                                                                                                                                                  note= "Second
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|ote= "Third IC loop"
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"Second EC loop"
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2000WO-US29601 99US-0427653 99US-0427859

99US-0428020. 99US-0428114. 99US-0429517. 99US-0429515. 99US-0429676. 99US-0429676. 99US-0424399. 2000US-0481794.

PHARMACIA & UPJOHN ŝ

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Wood LS,

7

2001-328653/34. )B; AAD06504.

Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophreni as well as for identifying compounds useful for treating schizophreni

Claim 1; Page 11-13; 215pp; English.

invention relates ç human G protein-coupled receptor (GPCR)

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RESULT AAG7165 ID AAG7165 ID AAG7165 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                08-OCT-1999;
24-FEB-2000;
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(YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                 Human GPCR polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                          06-MAR-2003
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                                                                                                                                                                                       n; GPCR; G protein coupled receptor; signal transduction; olfactory; development; gustatory; taste; fragrance, recent
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Pred. No. 5.9e-169;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                 158.
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Best Local S
Matches 316
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP9596-ABP95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrinsic and extrinsic ligands as bitter taste inhibitors, taste enhancers and fragrance improvers.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haga
         Human P835P protein
                            19-JUL-2002
                                               ABB95411;
                                                                ABB95411
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database global search for G protein-coupled receptors, encoded genes for studying in vivo signal transduction identifying targets for drug development
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13-FEB-2001;
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DB; ABZ42948.
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2001JP-0034434.
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                                                                Protein;
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Pred. No. 5.9e
1; Mismatches
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5.9e-169;
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                                                                                          Claim 2;
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(STOL/
(DAYC/
(VEDV/
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25-FEB-1998
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                                                                                                                                                                                                                                                        (CART,
                                                                                                                                                                                                                                                                                                     (FANG/)
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KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                               DILLON D C.
MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                STOLK J A.
DAY C H.
VEDVICK T S.
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DILLON
 Similarity
                           318
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                  New prostate-specific polynucleotides for diagnosing and diseases, in particular prostate cancer, and as markers f progression of cancer -

    cancer; prostate cancer; vaccine; cytostatic;
therapy.

                                                                                                                                                                                                                                                                                                                                                                CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                              Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                           SEQ ID NO 920; 87pp;
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2000US-0483672.
2000US-0536857.
2000US-0558100.
2000US-0570737.
2000US-0557793.
2000US-0605783.
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2000US-0657236.
2000US-0657236.
2000US-06585166.
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99US-0232149.
99US-0288946.
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                                                                                                           English.
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Carter D;
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99.8**%**; 99.7**%**;

Score Pred.

1614; DB 23; No. 5.9e-169;

Length 318;

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RESULT 12
AAU95746
ID AAU95746
XX AAU95746
XX AAU9574
AC AAU95
XX AOU95
XX AOU95
XX AOU95
XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; olfactory and pheromone G protein coupled; receptor; GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic; anorectic; taste; fragrance; food additive; cosmetic; cell migration; sterility; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; axonal growth; menstrual cycle; appetite sexual motivation; sexual attraction;
The invention relates to olfactory and Pheromone G-protein coupled receptor (GPCR) or a protein 95% identical to the GPCR, a specific active portion and its encoding polymucleotide. Also included are an agonist, antagonist or inhibitor of the GPCR or the polymucleotide, a vector
                                                                                                                                                                                           Novel pheromone G-protein coupled receptor and receptor-derived agonists, antagonists or inhibitors useful in food or cosmetic pror in the treatment or prevention of neurological disorders such anxiety and schizophrenia
                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                         Disclosure; Page 710-711; 833pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-2000; 2000EP-0870211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2001;
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DB; ABK68633.
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RESULT 13
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ID AAUS5181
XX AUS5
XX O8-MA
CT 08-MA
CX Human
KW Human
KW Odour
XX OOOU
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XX OOO
PN WO200
XX O2-JU
PR 22-JU
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human mammal comprising a partial or total deletion of the polynucleotide
cencoding the receptor and screening (detection and possibly, recovering)
of compounds which are known or not known to be agonist, antagonists or
inhibitors of natural compounds to the GPCR. The receptor-derived
agonists, antagonists, inhibitors or compounds are used as an
improvement, elimination or substitution of an existing taste and/or a
crimprovement of (or in) the food and/or cosmetic products. They can also be
improvement of the food and/or cosmetic products. They can also be
created in the preparation of medicament in the treatment and/or prevention
of a mammalian disorder, such as cell migration, sterility, psychotic and
neurological disorders, including anxiety, schizophrenia, manic
depression, depression, for promoting axonal growth, nerve cell
comnection and nerve regeneration for modulating male and female
commerciane functions, hormone production and the menstrual cycle, for the
prevention or the treatment by stimulation of several mammalian
behaviours, such as stimulation or suppression and for promoting or
suppressing chemical communication between organisms. The present
sequence is a human olfactory and pheromone GPCR protein sequence.
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Best Local Similarity
Matches 316; Conserv
                                                                                                                                                                               Human; olfactory G-coupled receptor; sensory perception of odourant; odour composition; taste composition.
                                                                                                                                                                                                                                   G-coupled olfactory receptor
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Pred. No. 5.9e-169;
1; Mismatches 0;
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22-JUN-2000; 2000US-213812P

22-JUN-2001; 2001WO-US20122

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RESULT 14
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XC ABU71
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of representing sensory perception of one or more odourants. The method comprises: (a) providing a representative class of n olfactory receptors or ligand binding domains (LBD) of these receptors; (b) measuring values X1 to Xn representative of at least one activity of one or more odourants selected from:
(i) binding one or more odourants to the LBD of at least one of the n olfactory receptors; (ii) activating at least one of the n olfactory receptors with the one or more odourants; and (iii) blocking at least one of the n olfactory receptors with the one or more odourants; and (c) generating a representation of sensory perception from the values X1 to Xn. The representation of the sensory perception of odourants is useful for the design and formulation of doour and taste compositions. AAUSS140-AAUSS33 represent human olfactory G-coupled receptor amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Representing sensory perception of one or more odourants identification and design of tastes and odours comprises representative group of n olfactory receptors -
 Prostate cancer; vaccine; gene therapy; cytostatic; immunogen; cancer; prostate specific antigen; PSA;
                                                Prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU85140-AAU85393
sequences of the j
                                                                              10-JUN-2003
                                                                                                                                         ABU71842 standard;
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MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEP

Best Matches Query Match

Local Similarity nes 316; Conser

Conservative

99.8%;

Score 1614; D Pred. No. 5.9e 1; Mismatches

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                                                                 The invention describes a fusion protein comprising at least one aminc acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This is the amino acid sequence of a prostate cancer therapy associated protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly seconds.
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04-OCT-2000; 2000US-0679272
28-MAR-2001; 2001US-0822827
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                                                seqdata.uspto.gov/sequence.html?DocID=US20020192763
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SKEIKY Y A W.

HEPLER W T.

HENDERSON R A.
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HARLOCKER S L.
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                                                                                                                                                                                  New isolated antigenic peptides e.g., for G (GPCR), useful for diagnosing and designing conditions in which GPCRs are involved, e.g.
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Search completed: February Job time : 44 secs ø 16:23:47

The present (a) any one acids. Also

invention describes antigenic peptides (I) comprising: of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino described: (1) an assay for the detection of a particular

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Listing first 45 summaries
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1. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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10621.628 Million ceil updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

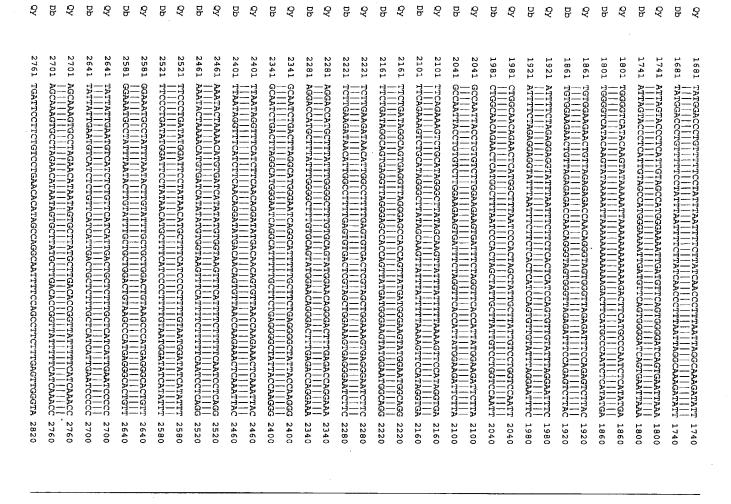
Afar DEH,

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The invention relates to a novel G-protein-coupled receptor up-regulated CC in prostate cancer, termed PHOR-1. The encoding cDNA is contained in CC plasmid designated pl01p3A11 deposited with ATCC as Accession No.pTA-312. CPOR-1 polypeptides and polypurcleotides are useful for diagnosing the CC protein or rectal cancer by determining and comparing the level of the CC protein or mRNA expression in test and normal tissue samples. CC protein or mRNA expression in test and normal tissue samples. CC Pharmaceutical compositions comprising PHOR-1 is useful for treating CC cancer. PHOR-1 proteins are useful for identifying ligands and other agents and cellular constituents that binds to PHOR-1 gene product and CC for generating antibodies which are useful in diagnostic, prognostic and CC ines expressing PHOR-1 are useful for identifying protein-protein cC interactions mediated by PHOR-1. The present sequence represents a cDNA canced in the formal control of the composition of the control o
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                                                                                                            CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACA
                                                                                                                                                                    GATGCTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG
                                                                                                                                                                                             GATGCTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG
                                                                                                                                                                                                                                                                                       ACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTTCCACTACCATCCAGTTT
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ABZ42822 standard;

04-MAR-2003 (first

Human ດ protein-coupled receptor Ls53440 nucleotide SEQ ID NO:433

RESULT 2
ABZ42822
ID ABZ42822
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AC ABZ4 G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; generation-calated disease; prowth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; ds

Homo sapiens.

19-DEC-2001; 2001WO-US50107

19-DEC-2000; 2000US-257144P

ი ც Roush CL, Brown

(LIFE-) LIFESPAN BIOSCIENCES

2003-046718/04. DB; ABP81974.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease cancer or autoimmune diseases

Disclosure; Fig 1; 523pp; English

	Qy 541 GTACTTACGTTGCCTCGTGTCACCAAAATTGGTGGCTGCTGTGGTGCGGGGGGGCTGCA	Qy 481 CTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACA	QY 421 GATGCTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTG	Qy 361 ACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATGCAGTTT	Oy 301 CTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCC	QY 241 TACCTTATTGCTGTGCTAAGTAACTTGACATCTACATTGTGCGGACTGAGCACAGC	QY 181 ATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTC	Qy 121 AGCTTCTTCATGATGGTGGATCCCAATGGCAATGACATCCCAGTGCTACATACTTCATCCTA	Qy 61 GGGGTCACACATTCCTTCCATACGGTTGAGCCTCTACCTGCCTG	Qy 1 CAGAGAGGCTGTATTTCAGTGCAGCCTGCCAGACCTCTTCTGGAGGAAGACTGGACAAAG	Query Match 100.0%; Score 3136; Best Local Similarity 100.0%; Pred. No. 0; Matches 3136; Conservative 0; Mismatches	Seque	GPCI	loss, epilepsy, asth hypotension, renal dany other disorder i	CC inflammation, allergies, Crohn's disease, diabetes, graft versus h CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, CC anxiety, depression, schizophrenia, dementia, mental retardation.	diseases, or atheroscleros		pr an	G a a	dî,
- Q	AY AFTERGETECTETEGTECGGGGGGGGTGCA 600 Db	540	480	CATCCAGTTT 420            ATCCAGTTT 420	360	300	240	180	120	60	DB 25; Length 3136; 0; Indels 0; Gaps 0;		o ABZ42869 encode	ea, hypertensic trauma, ulcers antibodies may	ies, Crohn's disease, diabetes, graft versus host disease, multiple sclerosis, pain, psoriasis, schizophrenia, dementia, mental retardation, memory			and in the production of specific Qy are also useful for detecting the CRs. The antigenic peptides for Db	 2019 to ABP88519) of 12-24 amino Db the detection of a particular candidate polypeptide in a sample.	ic peptides (I) comprising:
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16-MAR-2001; 2001US-276791P.
16-MAR-2001; 2001US-281922P.
24-APR-2001; 2001US-286514P.
30-APR-2001; 2001US-286514P.
30-APR-2001; 2001US-286514P.
30-APR-2001; 2001US-28659P.
Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated grare expressed in a prostate tissue
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Query Match
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Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;

The invention relates to isolated prostate-specific polymucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polymucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polymucleotide of the invention.

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09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-05970737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0605783.
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0685166.
                                                                                                                                                                                                                   Χu J,
                                                                                                                                                       New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                      Claim 1; Page 566-567; 579pp; English.
                                                                                                                                                                                 WPI; 2001-639232/73.
                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001; 2001WO-US09919
                                                                                                                                                                                                                                                                                                                                                                                    WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate cDNA sequence #594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS64175
                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2001.
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                                                                                                                                                                                              GR, Retu
                                                                                                                                                                                               Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTATGTGTTACACAGAGTAAATCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                                                                          Kalos MD;
Carter D;
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1020 CCTGTGTCTTGGAAGAAGTTATTTATTTTTAAAAAGTTCCATAGGTGATTCTCAGAA 2108 1020 CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA 2108 1020 CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCTATATTCTTATTTTAAAAGTTCCATAGGTGATTCTGATA 2168 2109 GTCTGCATAGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA 2168 11080 GTCTGCATAGGGCTTATAGCAAGTTATTTTTTTAAAAAGTTCCATAGGTGATTCTGATA 1139	AGAACTCATGGCTTTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCAATTA	1929 GAGGAGGTATTTAATTTCTTCTCACTCATCCAGTGTTGTATTTAGGAATTTCCTGGCAAC 1988 	1869 AACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTTCCAGAGTCTTACATTTTCTA 1928 	1809 TACAAGTATAAAAATTAAAAAAAAAAAAAGCTTCATGCCCAATCTCATATGATGTGGAAG 1868 	1749 CCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGGGTCA 1808 	1689 CTGTTTTTCCTATTTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTAC 1748 	1629 ATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGAGATATGGACC 1688 	1569 TTTTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGTAC 1628 	1509 ACCACATTGGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAGAAATAAT 1568 	1449 AGAATATAAATGAAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA 1508 	1389 GAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACAC 1448 	GCATTCTGAGATAA 1             GCATTCTGAGATAA 3	1269 TGCTACATATAATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT 1328 	1209 AAATATGAAACTGGTTGGGGAATCTCCATTTTTCAATATTATTTTCTTCTTTGTTTTCT 1268 	1149 TTTGGAAGACAGTATTCAGAAAAAAATTTCCTTAATAAAAAATACAACTCAGATCCTTC 1208 	1089 GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 1148 
AAA XXX XX	Db XX	dd d	g Qy	D 8	\$ 4g	B &	da Ao	da Yo	B &	da Yo	aa Ab	B &	dg Qy	dd YQ	Qy Db	کو کو
RESULT 5 AAH93939 ID AAH93939 standard; cDNA; 2061 BP. XX AC AAH93939; XX DT 04-OCT-2001 (first entry) XX	3069 GTACTATTGICTCAAG 3084 	3009 TCT	2949 GTT     1920 GTT	7 2889 TAAAACCCTCCCATGTGCAGCCTTTCATGTTGACATTAAATGTGACTTGGGAAGCTATGT 2948	7 2829 TTCTGGCCATTACTTCCAATGTGAGTGGAAGTGACATGTGCAATTTCTATACCTGGCTCA 2888	7 2769 TCTGTCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATTAAA 2828	7 2709 GCCTAGAACATAATAGTGCTTATGCTTGACAACCGGTTATTTTTCATCAAACCTGATTCCT 2768	2649 AAT     1620 AAT	2589 CTA     1560 CTA	2529 TAT     1500 TAT	2469 AAA     1440 AAA	н 2	. 2349 1320	1260	1200	Y 2169 GGCAGTGAGGTTAGGGAGCCACCAGTTATGATGGGAAGTATGGAATGGCAGGTCTTGAAG 2228 

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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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Kalos MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient for use in vaccines -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.
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                                                                             TGCTACATATAATTAATAACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT
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27-AUG-1999;
11-JAN-2000;
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                                                                                                                                                                                                                                                             sequence SEQ ID NO:17984
                                      ; 99JP-0248036.
; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprises a 3'-end sequence complementary to a colynucleotide which comprises a 3'-end sequence complementary to a colynucleotide which comprises a 3'-end sequence, where the colynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in CC the specification. The primers set useful for synthesising polynucleotides, and gene therapy. The primers are useful for synthesising polynucleotides, or particularly full-length cDNAs. The primers are also useful for the CC particularly full-length cDNAs. The primers allow obtaining of the full-length CDNAs and the protestar encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH3363 to AAH13628 and CC AAH3633 to AAH18742 represent human acond sequences; and AAH13629 to AAH13632 represent invention.
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Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 17984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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Sugiyama
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T, Wakamatsu
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A, Nagai I
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Otsuki
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Sequence 2061 BP: 612 A; 383 ü 399 ü 667 7, 0 other;

	Query Match	Match. 64.7%; Score 2028.4; DB 22; Length 2061;	
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Ś	1089	GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 1148	
日	63	GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT 122	
S	/ 1149	TTTGGAAGACAGTATTCAGAAAAAAATTTCCTTAATAAAAATACAACTCAGATCCTTC 1208	
밁	123	TTTGGAAGACAGTATTCAGAAAAAAAATTTCCTTAAT-AAAAATACAACTCAGATCCTTC 181	
8	/ 1209	AAATATGAAACTGGTTGGGGAAATCTCCAATTTTTTCAATATTATTTTTCTTCTTTGTTTTTCT 1268	
멍	182	AAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTTTTCTTCTTTGTTTTCT 241	
Ş	/ 1269	TGCTACATATAATTAATTAATACCCTGACTAGGTTGGGTTGGAGGGTTATTACTTTTCAT 1328	
뫄	242	TGCTACATATAATTAATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT 301	
Ś	/ 1329	TTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAA 1388	
닭	302	TTTACCATGCAGTCCAAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAA 361	
Ş	1389	GAATGGTACATCTAGAGAACATTTGCCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACAC 1448	
밁	362	GAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACGGCAAAGGAAAATAAACAC 421	
Ş	/ 1449	AGAATATAAATAAAATGAGATAAATCTAGCTTAAAACTATAACTTTCCTCTTCAGAACTCCCA 1508	
밁	422	AGAATATAATAAAAIGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA 481	

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GAGGAGGTATITAATITCTTCTCACTCATCCAGTGTTGTATTTAGGAATTTCCTGGCAAC
          CTATTTAATACTTGTATTTGCTGCTGGACTGTAAGCCCATGAGGGCACTGTTTATTATTG
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                                                                                                                                                                                                                                                                                                                                                                                                   present invention provides prostate-specific coding sequences and reacment rencoded proteins. These can be used in the diagnosis and treatment cancers, particularly prostate cancer. The present sequence is a cDNA
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SKEIKY Y A W.

HEPLER W T.

HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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RETTER M W.
STOLK J A.
DAY C H.
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Fanger
Li SX,
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or treating
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The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20020192763.

Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;

Ş 멼 5 밁 Ś 밁 S 밁 Ś Matches 2052; Query Match Best Local Similarity 1089 242 123 63 ω AAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTTCT TGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCAT TTTGGAAGACAGTATTCAGAAAAAAAATTTCCTTAATAAAAAATACAACTCAGATCCTTC GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT GTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACAT TTTGGAAGACAGTATTCAGAAAAAATTTCCTTAAT-AAAAATACAACTCAGATCCTTC Conservative 64.7%; 99.8%; <u>,</u> Score Pred. Mismatches No. 2028.4; 0 멂 25; Indels Length 2061; ω •• Gaps 1268 1148 301 1328 181 1208 122 241 82 1088

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SAXES	2109 GTCTGCATAGGGGCTTATAGCAAGTTATTTATTTTTAAAAGTTCCATAGGTGATTCTGATA 2168 
RESU AAAO ID	2049 CCTGTGTCTTGGAAGAAGTGATTTCTAGGTTCACCATTATGGAAGATTCTTATTCAGAAA 2108 
D 42	1989 AGAACTCATGGCITTAATCCCACTAGCTATTGCTTATTGTCCTGGTCCAATTGCCAATTA 2048 
B 5	1929 GAGGAGGIATTIAATTICTICICACCCATCCAGTGTGTATTTAGGAATTTCCTGGCAAC 1988 
B &	1869 AACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 1928 
S & &	1809 TACAAGTATAAAAATTAAAAAAAAAAAAAAGACTTCATGCCCAATCTCATATGATGTGGAAG 1868 
, B &	1749 CCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGGGTCA 1808 
? B &	1689 CTGTTTTCCTATTAATTTTCTTATCAACCCTTTAATTAGGCAAAGATATTATTAGTAC 1748 
) B &	1629 ATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGGACC 1688 -
) B &	1569 TITTCCTCTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTTGAAAAGAGTAC 1628
) B 8	1509 ACCACATIGGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAGAAGAAATAAT 1568 
) B Q	1449 AGAATATAAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTCAGAACTCCCA 1508 
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JLT 9 )9351 AÀA09351 standard; DNA; 1302 В₽

10-AUG-2000 (first entry)

G protein-coupled receptor protein 5 coding sequence.

GCRP-5; G protein-coupled receptor protein; antipsoriatic; antirheumatic; immunosuppressive; antiasthmatic; antianemic; antiarteriosclerotic; antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory; antigout; thyromimetic; haemostatic; virucide; hepatotropic; osteopathic; antiparasitic; immunostimulant; ss.

Homo sapiens

Location/Qualifiers 79..1035 /\*tag= a

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06-OCT-1998;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes human G-protein coupled receptor protein (GCRP) 5. The GCRP polypeptides, polynucleotides, antibodies, antagonists and agonists may be administered to human patients for the diagnosis, treatment and prevention of nervous system disorders (e.g. epilepsy, stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory disorders, complications of cancer, hemadialysis and extracorporeal circulation, and cell proliferative disorders. They are also used to treat or prevent disorders associated with decreased or increased expression or activity of GCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human G-protein coupled receptor proteins used in the diagnosis, treatment and prevention of nervous system disorders, autoimmune/inflammatory disorders, and cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1302 BP; 277 A; 346 C; 259 G; 420 T; 0 other;
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P-PSDB; AAY92365.
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Guegler KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                    112 TCACAGTTCAGCTTCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATAC 171
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CATGCCACAGTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGGCTGCTGTGGTGCGG
                                                                                                    ATCCAGTTTGATGCTTGTCTGCTACAGATGTTTGCCATCCACTCCTTATCTGGCATGGAA
                                                                                                                       ATCCAGTTTGATGCTTGTCTGCTACAGATTTTTGCCATCCACTCCTTATCTGGCATGGAA
                                                                                                                                                                              CTCATCTCCACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACC
                                                                                                                                                                                                                                          GAGCACAGCCTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATC 351
                                                                                                                                                                                                                                                                                                                                    TTCATCCTAATAGGCCT
                                                                                                                                                                                                                                                                                                                                                           TTCATCCTAATAGGCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTTGGCCTTCCCATTG 231
                                             recaeagraciaciacearacerriraacecrareresecarerereacecacracec
                                                                     TCCACAGTGCTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGC
                                                                                                                                                            CTCATCTCCACCTCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAATTCCACTACC
                                                                                                                                                                                                                    GAGCACAGCCTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATC
                                                                                                                                                                                                                                                                            TGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACT
                                                                                                                                                                                                                                                                                                                                                                                         TCACAGTTCAGCTTCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATAC 120
                                                                                                                                                                                                                                                                                                         TGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yue H, Lal P,
J, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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98US-0172211.
99US-0133585.
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Baughn MR,
                                                                                                                                                                                                                                                                                                                                  CCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1287.8;
Pred. No. 4.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4e-257;
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용양	<u> </u>	유 성	용 성	B 8	용 성	유 성	유 성	B 8	음 성	유 성	용 성	β. δ	용
1312 1260	1252 1200	1192 1140	1132 1081	1072 1021	1012 961	952 901	. 892 841	832 781	772 721	712 661	652 601	592 541	481
GGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAACT 1354 	TITCTTCTTIGTITTCTIGCTACATATAATTAATAATACCCTGACTAGGTIGTGGTIGGA 1311	TACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTAT 1251 	GATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAATTTCCTTAATAAAAA 1191 		GGAGTGAAGACAAAGGAGATTCGACAGGGCATCCTTCGACTTTTCCATGTGGCCACACAC 1071	CCCGTCATCTTGGCCAATATCTATCTGCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTAT 1011	GTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGÄCTCTCCGCTG 951		CTICTCATCTCCITCTCATATCIGCTIATTCTTAAGACTGTGTTGGGGCTTGACACGTGAA 831 		AATATCCTTTCCCATTCCTACTGCCTACACCAAGATGTCATGAAGCTGGCCTGTGATGAT 711	GGGGCTGCACTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCC 651 	L CATGCCACAGTACTTACGTTGCCTCGTGTCACCAAAATTGGTGTGGCTGCTGCTGGTGCGG 540

RESULT 10
AAS64174
ID AAS64
XX AAS64
AC AAS64
AC AAS64
XX 29-JA
DT 29-JA
DT Human
XX Human
XX Human
XX Homo
XX HOmo AAS64174 standard; 29-JAN-2002 AAS64174; (first CDNA; 1302 BP entry)

Human prostate cDNA sequence #593.

Human; prostate cancer; 93 cytostatic; immunostimulant;

Homo sapiens.

04-OCT-2001 WO200173032-A2

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Query Match
Best Local S
Matches 1300
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06-SEP-2000;
02-OCT-2000;
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated prostate-specific polymucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymucleotides and the antigen-presenting cells are useful for stimulating and/or expanding reells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polymucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fanger
Li SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 1302 BP; 277 A; 346 C; 259 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 566; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAU69951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORIXA CORP.
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ATCCAGTTTGATGCTTGCTACAGATTTTTTGCCATCCACTCCTTATCTGGCATGGAA
                                                                                                                                                                                                                                                    GAGCACAGCCTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTTCAGGCATTGACATC
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2000US-0568100.
; 2000US-0570737.
; 2000US-0593793.
; 2000US-06367183.
; 2000US-0636718.
; 2000US-0636718.
; 2000US-0651236.
; 2000US-0657279.
; 2000US-06851266.
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Pred. No. 4.4e-257;
0; Mismatches 2;
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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   RESULT 11
AAH93938
ID AAH93
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AC AAH93
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AC AAH93
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AC AAH93
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AC AAH93
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AC P835P
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                               P835P full length cDNA sequence
                                                                                          04-OCT-2001
                                                                                                                                                   AAH93938;
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient for use in vaccines -
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cytostatic; gene therapy; metastasis; ss.
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Query Match
                                                                                                                          progression of
                                                      The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatme of cancers, particularly prostate cancer. The present sequence is a cldescribed in the invention.
                                                                                                                 Claim
                                                                                                                                                                                                           Xu J,
Fanger
Li SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1999;
14-JAN-2000;
27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1997

01-AUG-1997

09-FEB-1998

25-FEB-1998

14-JUL-1998

23-SEP-1998

15-JAN-1999

09-AER-1999

13-JUL-1999
                                                                                                                                  New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer \,
                                Sequence 1302 BP;
                                                                                                                                                                                                                                                         (SKEI/)
(HEPL/)
(HEND/)
                                                                                                                                                                                                                                                                                                          (CART,
                                                                                                                                                                                                                                                                                                                               (KALO/
(FANG/
(RETT/
(STOL/
(DAYC/
(VEDY/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer;
gene therapy; ;
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                                                                                                                                                                                                      Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                      CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1999;
                                                                                                                                                                                                                                                                                                                                                                JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                              STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                               XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S
                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0605783.
; 2000US-0651236.
; 2000US-0651236.
; 2000US-0657279.
; 2000US-0679426.
; 2000US-0685166.
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2000US-0483672

2000US-056857

2000US-056810

2000US-0570737

2000US-0593793
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98US-0159812.

99US-0232149.

99US-0232146.

99US-0352616.

99US-0352616.
                                                                                                             NO 916; 87pp; English
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98US-0030607.
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                           277 A; 346 C; 259 G; 420 T; 0 other;
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        41.1%;
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       Score 1287.8;
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       DB
       24;
      Length 1302,
                                                                                                                                                                                                                    Kalos MD;
Carter D;
                                                              treatment is a cDNA
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GCTTCAGAGCCCTAGGTGTCAGTGATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCA
                                                                                                   CCGGTCATCTTGGCCAATATCTTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTAT
                                                  GGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACAC
                                                                                                                                                  GTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGCTG
                                                                                                                                                                              CCCGTCATCTTGGCCAATATCTATCTGCTGGTTCCTCCTGTGCTCAACCCAATTGTCTAT
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                                                                                                                                                                                               GCCCAGGCCAAGGCAITTGGCACTTGCGTCTCATGTGTGTGCTGTTGTTCATATTCTAT
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360 411 300 351 240 291 180 231 120 171 9 111

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Fanger G
Li SX,
Mcneill
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04-OCT-2000; 2000US-0679272.
28-MAR-2001; 2001US-0822827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA59982 standard; cDNA; 1302
                                                                               Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001US-0895793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                             (HEPL)
                                                                                                                                                                                                                                                                                                                                                                   (CART/
                                                                                                                                                                                                                                                                                                                                                                                                                      (VEDV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2002
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Yang -
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HENDERSON R A.
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HARLOCKER S L.
JIANG Y.
KALOS M D.
                                                                               Dillon DC,
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RETTER M W.
STOLK J A.
DAY C H.
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DILLON D C.
MITCHAM J L
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DAY C H.
VEDVICK T S.
                                                                                                                                                        MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                                                                                                                                                                                                                                                                            CARTER D.
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oon DC, Mitcham JL, Harlocker SL, Jiang Y, Retter MW, Stolk JA, Day CH, Vedvick TS, g A, Skeiky YAW, Hepler WT, Henderson RA, Houghton RL, Y De Bassols CV, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy associated cDNA #663.
                         Kalos MD;
Carter D;
Hural J;
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Matches 1300;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly seculate unit of the care them are the protein as the protein of the protein 
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                                       GGGGCTGCACTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCCTTCTGCCGCTCC
                                                                                                                                                           GGGGCTGCACTGATGGCACCCCTTCCTGTCTTCATCAAGCAGCTGCCCTTCTGCCGCTCC
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31-MAR-2000;
05-APR-2000;
06-APR-2000;
                                                                                                                                 anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                           30-MAR-2001;
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2000US-194614P.
2000US-195063P.
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GCCTCCCTGGTTTAGAAAGAGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACC GCCTCCCTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACC

120 244 60 184 0

TCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAG TCTTCATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAG Query Match Best Local S Matches 967

Local 967;

Similarity

30.8%;

Score 966.4; Pred. No. 1.5 Pred. No. 1.50 0; Mismatches

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Indels Length

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Gaps

Conservative

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125

Sequence

968

BP; 184 A; 281

<u>ე</u>

206

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297 T; 0

other;

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The invention relates to nucleic acid sequences (ABA81529-ABA81522) that CC (ABB44523-ABB44543). The isolated polypeptides CC (ABB44522-ABB44543). The isolated polypeptide having a sequence differing CC by no more than 15 % of amino acid residues from one of 22 amino acid CC sequences (or mature forms of the sequences) fully defined in the Specification and corresponding to human G-protein coupled receptor X (GPCRX) polypeptides. The polypeptides have potential cardiant, CC antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The CC polypeptides can be administered therapeutically, especially using gene CC therapy and expressing the encoding DNA in vivo, to treat or prevent CC GPCRX-associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders CC related to signal processing and metabolic pathway modulation (e.g. Cobsity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disorders, Huntington's disease, multiple CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's haematopoietic disorders, developmental diseases, neurological disorders, contental fungal protozoal and viral infections (e.g. Alzheimer's haematopoietic disorders, developmental diseases, neurological disorders, bacterial, fungal, protozoal and viral infections (e.g. with human content levels of the polypeptide expression to a disease associated with altered levels of the polypeptide in mammals (especially humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide (e.g. cellular receptors or downstream effectors) and/or agents (CC e.g. cellular receptors or downstream effectors) and/or agents (CC e.g. cellular receptors or downstream effectors) and/or agents
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06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
21-JUL-2000;
21-JUL-2000;
11-AUG-2000;
11-AUG-2000;
11-JUR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human G-protein coupled receptor X, GPCRX, polypeptide useful treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atheroselerosis, and to screen for antagonists agonists useful therapeutically
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Padigaru M, Mishnu VS,
Baumgartner JC, Gusev V
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2000US-19506PP.
2000US-195069P.
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2000US-221135P.
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Spytek KA,
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Li L;
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Human; GCPR; Human GPCR7b

polynucleotide

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G-coupled protein-receptor; cardiant; antiarteriosclerotic;

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06-APR-2000; 2000US-195068P.
06-APR-2000; 2000US-195069P.
06-APR-2000; 2000US-195070P.
06-APR-2000; 2000US-19510P.
21-JUL-2000; 2000US-219858P.
27-JUL-2000; 2000US-212354P.
28-JUL-2000; 2000US-212358P.
11-OCT-2000; 2000US-224588P.
11-OCT-2000; 2000US-239613P.
18-JAN-2001; 2001US-263508P.
23-JAN-2001; 2001US-263508P.
23-JAN-2001; 2001US-263508P.
23-JAN-2001; 2001US-263561P.
23-JAN-2001; 2001US-263561P.
23-JAN-2001; 2001US-263561P.
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05-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
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2000US-194614P.
2000US-195063P.
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(CURA-) CURAGEN CORP.

Majumder K, Padigaru M, Baumgartner JС, Vernet CAM, (
Mishnu VS, To
JC, Gusev VY; Tchernev Casman SJ, Chernev VT, Wolenc AR, Spytek KA, Spaderna Li L;

2001-639351/73.

New human G-protein coupled receptor X, GPCRX, polypeptide useful treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists agonists useful therapeutically

Claim 9; Page 57; 157pp; English

The invention relates to nucleic acid sequences (ABA81529-ABA81522) that encode G-coupled protein-receptor related polypeptides CC (ABB44522-ABB4443). The isolated polypeptide having a sequence differing CC by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the specification and corresponding to human G-protein coupled receptor X (GPCHX) polypeptides. The polypeptides have potential cardiant, CC antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The CC polypeptides can be administered therapeutically, especially using gene CC therapy and expressing the encoding DNA in vivo, to treat or prevent CC GPCHX-associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders (CC besity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple CC disease, parkinson's disorders, neurodegenerative disorders (e.g. Alzheimer's CC disease, parkinson's disorders, neurodegenerative disease), immune disorders, bacterial, fungal, protozoal and viral infections (e.g. with human CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used disgnostically to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide in mammals (especially humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide (e.g. cellular receptors or downstream effectors) and/or agents

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TAGGTGTCA	
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Search completed: February 9, 2004, 19:33:26 Job time: 808 secs

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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US-08-988-876-5
US-08-467-947A-2
US-08-465-990-3
US-08-465-990-3
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US-08-465-990-3
US-08-18-50-3
US-09-33-115-3
US-09-33-115-3
US-09-33-115-3
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## AL I GNMENTS

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APPLICANT: Jiang Yuqui
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APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Fenger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
                                                                                                                                                                                                                                         64 MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYV
                                                                                                                                                                                                                                                                                     67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
                                                                                                                                                                                                                                                                                                                                   VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL
                                                                                                                                                                                      AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
                                                MKLAYADTLPNVVYĞLTATLLVMGVDVMFISLSYFLİTRTVLQLPSKSERAKAFGTCVSH
                                                                          MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH
                                                                                                                                             ATCHPLRHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDV
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Pred. No. 1.3e-81;
5; Mismatches 67;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-980-2
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US-08-465-980-2
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Best Local Similarity
Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-UNN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 320 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
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ADDRESSEE: STUART & OLSTEIN
                                                             192
                                                                                           195 RVNVVYGLIVIISAIGLDSLLISFSYLLILKTYLGL-TREAQAKAFGTCVSHVCAVFIFY 253
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    Application US/08465980
    5756309

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New Jersey
VPFIGLSMVHRESKRRDSPLEVILANIYLLVPPVLNPIVYGVKTKBIRQRILRLFHVA 311
                                                       LPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFY 251
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amino acid
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                                                                                                                                                                                                                                                                              VLIGIPGLEKAHFWVGFPLLSMYVVAMCGNCIVVFIVRTERSLHAPMYLFLCMLAAIDLA 71
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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US-09-053-303-2
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Patent No. 5948890
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08,

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: ami
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REGISTRATION NUMBER: 3
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: New Jersey
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                 VELIGLSVVHREGNSLHPIVRVVMGDIYLLLEPVINPIIYGAKTKQIRTRVLAMFKIS 309
                                                                                                                             RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 253
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T: Ruben, Steven M.
INVENTION: HUMAN G
                                                     VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311
                                                                                         LPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFY 251
                                                                                                                                                                AAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADT 191
                                                                                                                                                                                                  ATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI 194
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STUART & OLSTEIN
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Pred. No. 2.6e-80;
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US-09-339-115-2
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
""" PHONE: 201-994-1700
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Best Local Similarity
Matches 177; Conserv
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Patent No. 6372891
GENERAL INFORMATION:
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
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ADDRESSEE: STUART & OLSTEIN
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                                                                                                   195 RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 253
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amino acid
                                 VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311
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                                                                         LPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAPGTCVSHIGVVLAFY 251
                                                                                                                                                                                                                                   LSTSTMPKILALFWFDSREISIEACLTOMFFIHALSAIESTILLAMAFDRYVAICHPLRH
VPLIGESVVHREGNSLHPIVRVVMGDIYLLEPPVINPIIYGAKTKQIRTRVLAMEKIS 309
                                                                                                                                                                                                                                                                                                                                                                                           59.6%; Score 964.5; DB 4 ilarity 59.4%; Pred. No. 2.6e-80; Conservative 54; Mismatches 66
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Li, Yi
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                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 320;
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GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 06-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 59.4 es 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STUART & OLSTEIN STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                         132
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                                     254 VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311
                                                                                    192 LPNVVÝGLTAILLVMGVDVMFÍSLSÝFLÍIRTÝVLQLPSKSERÁKAFGTĆVSHIGVÝLAFÝ 251
                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                            75 ISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRH 134
                                                                                                                                                                                                                                                                                                                                                   12 VLIGIPGLEKAHFWVGFPLLSMYVVAMCGNCIVVFIVRTERSLHAPMYLFLCMLAAIDLA 71
                                                                                                                                                                                                                                                                                                                                                                                        15 ILIGLEGLEBAQFWLAFFLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDIL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roseland
New Jersey
                                                                                                                          RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 253
                                                                                                                                                                       AAVLNNTYTAQIGIVAVVRGSLFFFFLFLIKKLAFCHSNVLSHSYCVHQDVMKLAYADT 191
                                                                                                                                                                                                                   ATVL/TLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI 194
                                                                                                                                                                                                                                                           LSTSTMPKILALFWFDSREISIEACLTOMFFIHALSAIESTILLAMAFDRYVAICHPLRH
VPLIGLSVVHREGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMEKIS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I: Rosen, Craig A.
I: Ruben, Steven M.
INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%; Score 964.5; DB 5; 59.4%; Pred. No. 2.6e-80; rative 54; Mismatches 66;
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RESULT 6 US-08-988-876-7 ; Sequence 7, Application US/08988876 ; Patent No. 6063596

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; CLONE: 32086
US-08-988-876-7
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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 294
                                   297
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                                                                                                                                                                                                                                                 127 AICHPLRHATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH 183
                                                                                                                                                                                                                                                                                                                       67 MLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
                                                                                                                                                                                                                                                                                      65 NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV 124
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NRDMKGALSRVIH 306
                                 TKEIRORILRLFH 309
                                                                                                                                                                            QDVMKLACDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAK 237
                                                                                                                                                                                                                 ATCFPL-HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDM 181
                                                                    AFSTCGSHLSVVSLFYGTVIGLYLC---SSANSSTLKDTVMAMMYTVVTPMLNPFIYSLR
                                                                                                     AFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPL-PVILANIYLLVPPVLNPIVYGVK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Bandman, Olga
Hillman, Jennifer L.
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Pred. No. 2.2e-31;
4; Mismatches 120;
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US-08-988-876-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application Patent No. 6063596
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lineal
IMMEDIATE SOURCE:
LIBRARY: GenBanl
CLONE: 1314667
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 31/.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
187 MKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCV 243
                                    125 AICYPLHYMVIMNPQLCSLLLLVSWIMSALHSLLQTLMVLRLSFCTHFQIPHFFCELNQM 184
                                                                      127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
                                                                                                       65 NISFVDICFTCTTIPKMIVNIQTQRKVITYESCIIQMYEFELFAGIDNFLITVMAYDRYM
                                                                                                                                             67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACILQIFAIHSLSGMESTVLLAMAFDRYV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                5 NDTRIPEFLLLGFSEEPKLQPFLFGLFLSMYLVTILGNLLLILAVSSDSHLHTPMYFFLA 64
                                                                                                                                                                                                            7 NESSATYFILIGLEGLEEAQFWLAFPLCSLYLIAVLGNLTIYIVRTEHSLHEEMYIFLC 66
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                                                                                                                                                                                                                                                                        Similarity
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Bandman, Olga
Hillman, Jennifer L.
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                                                                                                                                                                                                                                               24.4%; Score 394.5; DB 3;
29.0%; pred. No. 2.1e-28;
29.0%; mismatches 126;
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SHVCAVFIFYVPFIG--LSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIR 301

IQLACSDTFLNNMMLYFAAILLGVAPLVGVL--YSYFKIVSSIRGISSAHSKYKAFSTCA

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US-08-988-876-6
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Best Local S
Matches 94
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Patent No. 6063596
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNMBER: 26,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-655-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: -US/08/00^

FILING DATE: Here...
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                Local L
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CLONE: 205814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                         Similarity
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     CEPNOVIQUICSDAFLNDLVIYFTLVLLATVPLAG--IFYSYFKIVSSICAISSVHGKYK
                                    CLHQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTR-EAQAK 237
                                                                                                          YVAICHPLRHATVLTLP----RVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSY 180
                                                                                                                                           LSNLSFVDICFISTTVPKMLVNIQTQNNVITYAGCITQIYFFLLFVELDNFLLTIMAYDR 122
                                                                                                                                                                                                                   SSNRTRVSEFLLLGFVENKDLOPLIYGLFLSMYLVTVIGNISIIVAIISDPCLHTPMYFF
                                                                                                                                                                                                                                                   NGNESSATYFILIGLEGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIF
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                                                                        YVAICHPMHYTVIMNYKLCGFLVLVSWIVSVLH--ALFQSL--MMLALPFCTHLEIPHYF
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3174 Porter Drive
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Bandman, Olga
Hillman, Jennifer L.
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                                                                                                                                                                                                                                                                                        23.7%; Score 383; DB 3; 28.3%; Pred. No. 2.6e-27; tive 73; Mismatches 133
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                                                                                                                                                                                                                                                                                        133;
                                                                                                                                                                                                                                                                                                                          Length 333;
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APPLICANT: Reed, Kandall
APPLICANT: Yau, King-Wai
APPLICANT: Yau, King-Wai
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
ITILE OF INVENTION: Olfactory Receptor Expession Libraries
ITILE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
FRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 313
TYPE: PRT
                                                                                                                        RESULT 10
US-08-467-948A-2
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US-09-465-901-48
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                                                                                       Sequence 2, Application US/08467948A Patent No. 5998164
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                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                              298 Q 298
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                                                                                                                                                                                                                                                                   242 HIIVVSLFYGSCI--FMYVRSGKNGQGEDHNKVVALLN--TVVTFTLNFFIYTLRNKQVK
                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NFAMLEIWFTSVIFPKMLTNIITGHKTISLLGCFLQAFLYFFLGTTEFFLLAVMSFDRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 NESSATYFILIGLEGLEEAQFWLAFELCSLYLIAVLGNLTIIYIVRTEHSLHEFMYIFLC 66
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                                                                                                                                                                                                                                                                                                                                       MELICADTSLVEFLGFVIANFSL-LGTLAVTATCYGHILYTILHIPSAKERKKAFSTCSS
                                                                                                                                                                                                                                                                                                                                                                          MKLACDDIRVNVVYGLIVIISAIGLDSLLISFS-YLLILKTVLGL-TREAQAKAFGTCVS
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LI, YI
CAO, LIANG
NI, JIAN
GENTZ, REINER
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RESULT 11
US-08-467-947A-2
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                                                          Sequence 2, Application US/08467947A Patent No. 6090575
GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.114000:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  APPLICANT:
APPLICANT:
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TOPOLOGY: line
MOLECUT
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MEDIUM TYPE: FLOPPY |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                       184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 22.7%; Score 367; DB 2; Similarity 32.2%; Pred. No. 6.5e-26; 94; Conservative 61; Mismatches 121
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                                                                                                                                                                                                   FSTCSSHLCVVGLFFGSAIVMYMAPK-SRHPEEQQKVLFLILQFLSTPMLKP
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LI, YI
CAO, LIANG
NI, JIAN
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SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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Local Similarity
Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEPPE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 296 amino TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                   183
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                                                                                                                                                      124 DRYVAICHPLRYFIIMTWKVCITLGITSWTCGSLLAMVHVSLILRLPFCGPREINHFFCE 183
                                                                                                                                                                                                                                  64 FFLSHLAVVNIAYACNTVPQMLVNLLHPAKPISFAGCMTLDFLFLSFAHTECLLLVLMSY 123
                                                                                                                                                                                                                                                                     63 IFLCMLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQIFAIHSLSGMESTVLLAMAF 122
                                                                                                                                                                                                                                                                                                                                                                                          94; Conservative
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T: 1100 NEW YORK AVE.,
WASHINGTON
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                                                                                                              HQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLL--ILKTVLGLTREAQAKA 238
                                                                                                                                                                                                                                                                                                                                                   NESSATYFILIGL---PGLEEAQFWLAFPLCSL-YLIAVLGNLTIIYIVRTEHSLHEPMY
                                   FGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNP 290
                                                                                                                                                                                            DRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCL 182
                                                                                                                                                                                                                                                                                                             NOTMVTEFLLLGFLLGPRIQ----MLLFGLFSLFYVFTLLGNGTILGLISLDSRLHTPMY
FSTCSSHLCVVGLFFGSAIVMYMAPK-SRHPEEQQKVLFLILQFLSTPMLKP
                                                                         ILSVLRLACADTWLNQVVIFEACMFILVGPLCLVLVSYSHILGGILRIQSG---EGRRKA
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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                                                                                                                                                                                                                                                                                                                                                                                      22.7%; Score 367; DB 3; 32.2%; Pred. No. 6.5e-26; tive 61; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides Encoding Human G-Protein
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                                                                                                                                                                                                                                                                                                                                                                                        121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 296;
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291
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RESULT 12 US-08-465-980-3

Sequence 3, Application US/08465980 Patent No. 5756309

GENERAL INFORMATION:

APPLICANT:

Soppet, Li, Yi

Daniel R.

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RESULT 13
US-09-053-303-3
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                                                                                                             Sequence 3, Application US/09053303
Patent No. 5948890
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPDATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CARELLA, BYRNE,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI
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Pred. No. 3.9e-25;
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RESULT 14
US-09-339-115-3
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Best Local Similarity 36.5%,
Marches 93, Conservative (
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STUART & OLSTEIN
STRRET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                       233
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                                                                                                                                                                                                                                                                                                                                                                                       14 FILIGLEGLEEAQFWLAFELCSLYLIAVLGNLTIIYIVRTEHSLHEEMYIFLCMLSGIDI
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New Jersey
                                                                                                         HVCAVFIFYVPFIGL 259
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                                                                                                                                                                                                             HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDMSALLKLA 177
                                                                                                                                                                                                                                             HATVLTLERVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 190
                                                                                                                                                                                                                                                                                                                                                       FILLGLFIQPÉQQNLCYALFLAMYLTTLLGNLLITVLIRLDSHLHTPMYLFLSNLSFSDL
                                                                     HLSVVSLFYGTVIGL 247
                                                                                                                                         FSDTRVNEWVIFIMGGLILVÍ-----PFLLÍLGSÝARÍVSSILKVPSSKGICKAFSTCGS
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Sequence 3, Application US/09339115
Patent No. 6372891
GENERAL INFORMATION:

Soppet, Daniel Li, Yi

APPLICANT: ROSEN, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8

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RESULT 15
PCT-US95-07093-3
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                                                                                                                                                                         Sequence 3, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local |
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                       CORRESPONDENCE ADDRESS:
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STREET: 7 Roseland
CITY: Roseland
TTATE: New Jersey
TTSA
                                                        NPPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
LITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
UMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferraro, Gregory
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                               233 HLSVVSLFYGTVIGL 247
                                                                                                                                                                                                                                                                                                                                    245 HVCAVFIFYVPFIGL 259
                                                                                                                                                                                                                                                                                                                                                                      178 FSDTRVNEWVIFIMGGLILVI----PFILILGSYARIVSSILKVPSSKGICKAFSTCGS
                                                                                                                                                                                                                                                                                                                                                                                                            191 CDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 HATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CFSSVTIPKLLONMONODPSIPYADCLTOMYFFLLFGDLESFLLVAMAYDRYVAICFPL- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 LISTSSMPKMLAIFWENSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 FILIGLEGLEEAQFWLAFELCSLYLIAVIGNLTIIYIVRTEHSLHEEMYIFLCMLSGIDI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
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                                                                                                                                                                                              Application PC/TUS9507093
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E: STUART & OLSTEIN
6 Becker Farm Road
                                                                                                                                      Soppet, Daniel R.
Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
CARELLA, BYRNE, BAIN, STUART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-994-1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferraro, Gregory REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             Local
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233
                                                                             178
                                                                                                                  191
                                                                                                                                                     120 HYTAIMSPMLCLALVÄLSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDMSALLKLÄ 177
                                                                                                                                                                                                                                                                                                                                                 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
                                                                                                                                                                                                                                                                      74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 36.5
93; Conservative
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                                                                                                              CDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
HLSVVSLFYGTVIGL 247
                                     HVCAVFIFYVPFIGL 259
                                                                        FSDTRVNEWVIFIMGGLILVI-----PFLLILGSYARIVSSILKVPSSKGICKAFSTCGS
                                                                                                                                                                                         HATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 190
                                                                                                                                                                                                                                CFSSVTIPKLLONMONODPSIPYADCLTOMYFFLLFGDLESFLLVAMAYDRYVAICFPL- 119
                                                                                                                                                                                                                                                                                                           FLLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLITVLIRLDSHLHTPMYLFLSNLSFSDL
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                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                      Score 357.5; DB 5;
Pred. No. 3.9e-25;
6; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                        Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 247;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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9

Search completed: February Job time : 22 secs ø 2004, 16:26:17

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Perfect score:
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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1617
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	

No.	Score	Query	Length	BG	ij	Description
۲	1617	100.0	317	15	US-10-205-823-443	Sequence 443. Ar
2	1617	100.0	318	15	US-10-001-469-2880	2880
ω	1614	99.8	317	12	US-10-295-027-873	
4.	1614	99.8	317	12	US-10-292-798-746	746
v	1614	99.8	318	9	US-09-759-143-920	Secuence 920 Apr
σ	1614	99.8	318	9	US-09-780-669-920	Sequence 920. App
7	1614	99.8	318	φ	US-09-822-827-920	Sequence 920. App
00	1614	99.8	318	10	US-09-886-055-91	Sequence 91. Apr
9	1614	99.8	318	10	US-09-895-793-920	Sequence 920. Ap
10	1614	99.8	318	10	US-09-895-814-920	Sequence 920, Ap
11	1614	99.8	318	11	US-09-966-459A-2	Sequence 2. Appli
12	1614	99.8	318	11	US-09-804-291-91	Sequence 91, App
13	1614	99.8	318	12	US-10-017-161-868	Sequence 868, App
14	1614	99.8	318	12	US-10-144-678A-920	Œ
15	1614	99.8	318	12	US-10-294-025-920	

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-10-012-896	-09-981-566A-5	-10-005-041A-4	-10-387-629-20	-10-025-806-3	-10-431-842	-10-044-643-6	0-294-025-52	-10-144-6	-09-804-291-8	-09-895-814-5	-09-895-793-52	S-09-968-033C-	S-09-886-055-8	09-822-827-52	-09-780-669-52	-09-730-018-	-09-759-143-52	-10-024-399-18	-10-005-041A-4	10-114-6	-10-001-469-288	-10-001-469-288	-10-001-469-288	-10-001-469-288	-10-044-643-3	-10-044-643-28	-10-225-567A-	-10-012-896-92	7-640-44
Sequence 527, App	equence 55,	equence 41,	equence 200, Ap	equence 34, App	equence 7, Appl	equence 65, App	equence 527, Ap	quence 52	equence 83, App	equence 527, Ap	equence 527, Ap	equence 4,	equence 83, App	equence 527	quence 527	equence 7, 1	equence 527	equence 18	equence 42,	Sequence 8894, Ap	equence 288	equence 288	equence 288	quence 288	equence 30,	equence 28,	quence 434	equence 920	TICE 25

## ALIGNMENTS

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TYPE: PRT ORGANISM: Homo sapiens	SEQ ID NO 443	SOFTWARE: FastSEQ for Windows Version 4.0	NUMBER OF SEQ ID NOS: 455	PRIOR FILING DATE: 2002-03-05		PRIOR FILING DATE: 2001-12-12	PRIOR APPLICATION NUMBER: 60/341,746	PRIOR FILING DATE: 2001-09-25	APPLIC	PRIOR FILING DATE: 2001-08-22	PRIOR APPLICATION NUMBER: 60/314,356	PRIOR FILING DATE: 2001-07-25	PRIOR APPLICATION NUMBER: 60/307,982	CURRENT FILING DATE: 2002-07-25	CURRENT APPLICATION NUMBER: US/10/205,823	FILE REFERENCE: MRI-044	THERAPY OF PROSTATE CANCER	INVENTION: METHODS FOR IDENTIFICATION, ASSE	¥	••	•••	e Glatt, Karen		APPLICANT: Kamatkar, Shubhangi			APPLICANT: Gannavarapu, Manjula			APPLICANT: Schlegel, Robert	GENERAL INFORMATION:	Publication No. US20030108963A1	Sequence 443, Application US/10205823	US-10-205-823-443	RESULT 1

US-10-205-823-443

Query Match Best Local

Local

317; Conservative

0; Mismatches

Length

100.0%; Similarity 100.0%;

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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20024.30
CURRENT APPLICATION NUMBER: US/10/001,469
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/291,118
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/291,28
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2888
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2880
LENGTH: 318
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                                                                                                                                                    ; OTHER INFORMATION: Description of Unknown Organism: 101P3A11 encoded amino; OTHER INFORMATION: acid sequence
US-10-001-469-2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-001-469-2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                           Query Match
Best Local Sim
Matches 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2880, Application US/10001469 Publication No. US20030091562A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JAKOBOVITS, AYA APPLICANT: RAITANO, ARTHU APPLICANT: AFAR, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                           ORGANISM: Unknown Organism FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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                                                                                           Similarity
                      WVDPNGNESSATYFILIGLPGLEBAQFWLAFPLCSLYLIAVLGNLTIIXIVRTEHSLHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAITANO, ARTHUR
AFAR, DANIEL
SAFFRAN, DOUGLAS
HUBERT, RENE
FARIS, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
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MVDPNGNESSATYFILIGLEGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEP 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHALLITA-EID, PIA
                                                                   100.0%; Score 1617; ilarity 100.0%; Pred. No. 5. Conservative 0; Mismatches
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Pred. No. 5.9e-150;
); Mismatches 0;
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                                                                                         .9e-150;
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Matches Query Match

Local Similarity es 316; Conserv

99.8%; Score 1614; DB 12; 99.7%; Pred. No. 1.2e-149; vative 1; Mismatches 0;

Length 317; Indels

0;

0,

```
APPLICANT: Macray, Loridan.

APPLICANT: Watson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: EoS Biotechnology, Inc.

ITILE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE REFERENCE: 018501-012500US

CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT APPLICATION NUMBER: US 09/663,733

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-09

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR AP
; TYPE: PRT ; ORGANISM: Homo sapiens US-10-295-027-873
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                                                                                                   Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 873
LENGTH: 317
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APPLICANT: Azir, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
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Mack, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10295027
5. US20030232350A1
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Sequence 746, Application US/10292798

Publication No. US20030235833A1

GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: JP 2007-11-18
PRIOR APPLICATION NUMBER: JP 2007-13-18
PRIOR APPLICATION NUMBER: JP 2007-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PRIOR TILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PRIOR TILING Ver. 2.1
TYDE: PRT
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US-10-292-798-746
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Best Local Similarity 99.7%;
Matches 316; Conservative 7
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L0-292-798-746
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                       241
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TCVSHVCAVFIEYVPFIGLSMVHRESKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI
                                                                                                                                                                         MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAM
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Pred. No. 1.2e-149;
1; Mismatches 0;
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SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORCANISM: Homo sapiens
US-09-759-143-920
   RESULT 6
US-09-780-669-920
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US-09-759-143-920
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                RORILRLFHVATHASEP 318
                                                                                    RORILRLFHVATHASEP 317
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
NUMBER OF SEQ ID NOS: 934
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US20020022248A1
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   TCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI
                                    TCVSHVCAVEIFYVPFIGLSMVHRESKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKBI 300
                                                                                                                                                               CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
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99.7%; Pred. No. 1.2e-149;
7ative 1; Mismatches 0;
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT APPLICATION STANDARD: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 920
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
OPTANISM: Homo sapiens
                                                                                                                              RESULT 7
US-09-822-827-920
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US-09-780-669-920
Sequence 920, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Best Local :
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Carter, Darrick
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ick, Thomas S.
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99.7%;
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Pred. No. 1.2e-149;
1; Mismatches 0;
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CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-920
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US-09-886-055-91
; Sequence 91, Appli
; Patent No. US20020
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; TYPE; PRT
; ORGANISM: Homo sapiens
US-09-886-055-91
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GENERAL INFORMATION:

APPLICANT: STRVER, LUBERT

APPLICANT: ZOZULYA, SERGEY

APPLICANT: ZOZULYA, SERGEY

TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

FILE REFERENCE: 078003-0277150

CURRENT APPLICATION NUMBER: US/09/886,055

CURRENT FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: 60/213,812

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 522

SOFTWARE: PATENTIN OP: 221
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 91
                                                                                                                                                                      Matches 316;
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Best Local Similarity
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Pred. No. 1.2e-149;
1; Mismatches 0;
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APPLICANT: Foy, Teresa

APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C2

CURRENT APPLICATION NUMBER: US/09/895,793

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 920

SEQ ID NOS: 982

TYPE: PAT

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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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US-09-895-793-920
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US-09-895-793-920
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                                                                   MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAM
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                               AFDRYVAICHELRHATVLTLERVTKIGVAAVVRGAALMAPLEVEIKQLEFCRSNILSHSY 180
                                                                                                                                         MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEP
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Hepler, William T.
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Vedvick, Thomas S
Carter, Darrick
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b. US20020192763A1
                                                                                                                                                                                                         99.8%; Score 1614; DB 10; ilarity 99.7%; Pred. No. 1.2e-149; Conservative 1; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-920
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US-09-895-814-920
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TITLE OF INVENTION: COMPOSTITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 920
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Matches
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hes 316;
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                                                                                                                                                                                                                                                                                        Similarity
                                                                                      AFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPPCRSNILSHSY 180
                                                                                                                                  MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAM
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CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
                           CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFG
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Dillon, Davin C.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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Harlocker, Susan L.
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Kalos, Michael D.
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o. US20020193296A1
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Pred. No. 1.2e-149;
1; Mismatches 0;
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APPLICANT: KCHACKER, M.G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY4,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG
FILE REFERENCE: D0039NP
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,833
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/261,776
PRIOR APPLICATION NUMBER: 60/361,776
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/305,351
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PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 60
CORPWANDE: DESCRIPTION OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SECURITY OF SEC
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; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-459A-2
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US-09-966-459A-2
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APPLICANT: MINTIER, G.
APPLICANT: RAWANATHAN, C.S.
APPLICANT: HAWKEN, D.R.
APPLICANT: CACACE, A.
APPLICANT: BARBER, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.8%;
Best Local Similarity 99.7%;
Matches 316; Conservative
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Pred. No. 1.2e-149;
1; Mismatches 0;
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Sequence 91. Application US/09804291
Publication No. US20030088059A1
GENERAL INFORMATION:
APPLICANT: ZOZULA, SERGEY
FITTLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCO
FILE REFERENCE: P0278005
CURRENT APPLICATION NUMBER: US/09/804,291
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/198,474
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/198,474
PRIOR APPLICATION NUMBER: 60/198,35
PRIOR APPLICATION NUMBER: 60/198,35
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,33
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,33
PRIOR APPLICATION NUMBER: 60/203,33
PRIOR APPLICATION NUMBER: 60/205,534
PRIOR APPLICATION NUMBER: 60/205,534
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/266,862
PRIOR FILING DATE: 2000-08-27
NUMBER: FOR PRIOR FILING DATE: 2001-02-07
NUMBER: FOR PRIOR FILING DATE: 2001-02-07
NUMBER: PRIOR FILING DATE: 2001-02-07
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NUMBER: PRIOR FILING DATE: 2000-08-02-07
NUMBER: PRIOR FILING DATE: 2000-08-0
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US-10-017-161-868
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                                                                                                                                    Sequence 868, Application No. US20
GENERAL INFORMATION
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Best Local S
Matches 316
APPLICANT: SUWA, MAKIKO
APPLICANT: ASIANA, VUTSKA
APPLICANT: AKIYAWA, VUTSKA
APPLICANT: ABURATANI, HIROYUKI
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Pred. No. 1.2e-149;
1; Mismatches 0;
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RESULT 14
US-10-144-678A-920
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; ORGANISM: Homo sapiens
US-10-017-161-868
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FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 868
LENGTH: 318
TITLE OF INVENTED RECEPTORS
LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 920, Application US/10144678A Publication No. US20030157089A1
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Best Local Similarity 99.7%;
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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                                                   Houghton, Raymond L. Vinals y de Bassols, Foy, Teresa M.
                                                                                                                                                                                                                                                                                                                                                                                   Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                   Watanabe, Yoshihiro
Deng, Ta
                                                                                                                               Hepler, William T.
Hural, John
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Carter, Darrick
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                                                                                                             McNeill, Patricia D.
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                                                                                                                                                                                    Wang, Aijun
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 COMPOSITIONS
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Pred. No. 1.2e
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 AND METHODS FOR THE THERAPY AND
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-920
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US-10-294-025-920
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
                                                                                                                                               Query Match
Best Local Similarity
Matches 316; Conserv
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CURRENT APPLICATION NUMBER: US/10/144,
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 920
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APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427029
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TYPE: PRT
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                         61 MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTTIQFDACLLQIFAIHSLSGMESTVLLAM
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MYIFICMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAM
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5. US20030185830A1
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                                                                                                                                           Score 1614; DB 12;
Pred. No. 1.2e-149;
1; Mismatches 0;
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Pred. No. 1.2e-149;
1; Mismatches 0;
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1 MYDDNGNESSATYFILIGLE......KEIRQRILRLFHVATHASEP 317
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Query Match 99.8%; Score 1614; DB 4; Length 317; Best Local Similarity 99.7%; Pred. No. 1.6e-135; Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps		DR PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.				EMBL: AB065787; BAC06006.1;	EMBL; BC022401; AAH22401.1;	receptor genes."; Submitted (JUL-2001) to the EMBL/GenBa	"Genome-wide discovery and analysis	Tsutsumi S., Aburatani H., Asai K., Ak			[2]						NCBI TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae;		Homo sapiens (Human).	Hypothetical protein (Seven	01-MAR-2003 (TrEMBLrel. 23, Last	01-JUN-2002 (TrEMBLrel. 21,	DT 01-JUN-2002 (TrEMBirel. 21, Created)		TCB6	RESULT 1
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Matches 295;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
01factory receptor MOR18-1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat.
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AX1072993; AAL60656.1; -
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GFCRHODDPSN.
PROSTITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSTITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.
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"The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                           93.5%; Score 1512; DB 11; 93.4%; Pred. No. 1.9e-126; 93.4%; Pred. No. 1.9e-11; tive 10; Mismatches 11;
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Matches 183
                                                                                                                                                               the RIKEN Genome Exploration Research Groumanaysis of the mouse transcriptome based 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

EMBL; AX073011; AAL560674.1; ---
EMBL; AX073614; AAL560674.1; ---
EMBL; AX028467; BAC25966.1; ---
EMBL; AX028467; BAC25966.1; ---
EMBL; AX036356; BAC25996.1; ---
EMBL; AX036356; BAC25996.1; ---
EMBL; AX036356; BAC25996.1; ---
EMBL; BX02076; GPCR_Rhodpsn.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PR00237; GFPCMPHODOPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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"The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
[2]
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN=C57BL/6J; TISSUE-Cerebellum,
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and genetic characterization of an evolutionarily human olfactory receptor that is differentially expressed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21564169; PubMed=11707321; Yuan T.T., Toy P., McClary J.A., Lin Kretschmer P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 278:41-51(2001).
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                                              Score 985; DB
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53; Mismatches
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Q8VF09;
O1-MAR-2002 (TrEMBLrel 20, 1
O1-MAR-2003 (TrEMBLrel 20, 1
O1-MAR-2003 (TrEMBLrel 23, 1
O1factory receptor MOR18-3.
Mus musculus (Mouse)
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY073732; AAL61395.1; -- Interpro; IPR000276; GPCR_Rhodpsn.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                       HQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGT
                                                                                                                                                                                                                                                                                                                                               FLAMLSTIDLVLSSVTMEKMASLFLTGIQEIEFNICLTQMFLIHALSAMESAVLLAMAF
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           CISHLCAVLVFYVPLIGLSVVHRLG-GPTSLVHVIMANIYLLLPPVVNPIVYGAKTKEIR
                                            CVSHVCAVFIFYVPFIGLSMVHRFSXRRDSPLPVILANIYLLVPPVLNPIVYGVKTKBIR 301
                                                                                                                                                                                                                                                                       DRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCL
                                                                                                                                                                                                                                      DRFVAICYPLRHASVLTGTTVAKIGLASLARGFVFFFPLFFLLKRLSYCQTHTVTHSFCL
                                                                                                                                                                                                                                                                                                                                                                                IFLCMLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQIFAIHSLSGMESTVLLAMAF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLACDDIRVNVVYGLIVIISAIGLDSLLISESYLLILKTVLGL-TREAQAKAFGTCVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AA; 35612 MW; D40302782D4B2FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Y receptor gene :
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59.0%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 965.5; DB 11;
Pred. No. 7.3e-78;
7; Mismatches 66;
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Best Local S
Matches 179
Q8VH05
Q8VH05;
Q8VH05;
Q8VH05;
Q1-MAR-2002 (TrEMBLrel. 20, Cresol-MAR-2002 (TrEMBLrel. 23, Lassol-MAR-2003 (TrEMBLrel. 23, Lassol-MAR-2003 (TrEMBLrel. 23, Lassol-MAR-2004) (Mouse MOR10-1.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8NGF3;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1;
PROSITE; PS00237; G PROTEIN_RECEP_F1_2;
Receptor; Transmembrane.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2002 (TrEMBirel. 22, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation updat
Seven transmembrane helix receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB065855; BAC06073.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor genes."
Submitted (JUL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
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179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHLCAVLVEYVPLIGLSVVHRLG-GPTSLLHVVMANTYLLLPPVVNPLVYGAKTKEICS
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58.5%; Pred. No. 2.3e-75;
tive 52; Mismatches 72
                                                                                      Created)
Last sequence update)
Last annotation update)
        Craniata;
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           Vertebrata;
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QBVH11;
QBVH11;
Q1-MAR-2002 (TrEMBLrel. 20, Clored Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072977; AAL60640.1; -. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                     Zhang
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SEQUENCE
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=10090
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"The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
                                                                                  Adams M.;
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00237; G PROTEIN RECEP_F1_1; PROSITE; PS50262; G PROTEIN RECEP_F1_2;
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NCBI_TaxID=10090;
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                                                                                                                                           1g X., Fires
3 olfactory
6. Neurosci.
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                                                                                                                                                                                     Firestein
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Conservative 6
                                                                                                                                                receptor gene 0:0-0(2002).
                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                     S.J.;
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Pred. No. 2.4e-73;
5; Mismatches 74;
                                                                                                                                                                 superfamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local S
Matches 164
                                                                                                                                                                  Matches
                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                     receptor genes.";
Submitted (JTL-2001) to the EMBL/GenBank/DDBJ da
EMBL; AB065794; BAC06013.1;
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PP00001; 7tm.1; 1.
Pfam; PP00037; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS0237; GPROTEIN_RECEP_F1 2; 1.
Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBNGKO PRELIMINARY; PRT; 314 AA.
QBNGKO;
QDNGKO;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Seven transmembrane helix receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Suwa M., Sato T., Okouchi I., Arita M., Futami K.,

Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;

"Genome-wide discovery and analysis of human seven
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SEQUENCE
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
PROSTTE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
LCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDR
                                                                  VSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKBIRQ
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                                                                                                                                                                                                                                                         314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                    35012 MW; 97DD37E1F38E976C CRC64;
                                                                                                                                                                                    55.2%;
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                                                                                                                                                           63;
                                                                                                                                                                                    Score 892.5;
Pred. No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Ve
Catarrhini;
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                    .2e-71;
                                                                                                                                                                                                          DB 4;
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Matches 158
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01-MAR-2002 (TrEMBLrel 20, I

01-MAR-2003 (TrEMBLrel 23, I

Olfactory receptor MOR7-1.

Mus musculus (Mouse)
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Zhang X., Firestein S.J.;
"The olfactory receptor go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                     LCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDR
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                                                                                                                                                                     DVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLG-LTREAQAKAFGTCV
                                                                                                                                                                                                                                                                                                                                                                                 NSSLQKATEF-LTGFQGLEEFHGWISIPFCSIXLIVILGNLTILHVIRTDATLHBPMYYF
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                                               SHICAVLLEYIPMIGLSLVHREGEHLPRIVHLLMSYVYLLVPPLMNPIVYSIKTKQIRQR
                                                                                     SHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQR
                                                                                                                                                                                                              YVAICNPLRYSTILTPRRIVKMGLSSVLRSALLILPLPFFLLKRFHYCRSHVLAHAYCLHL
                                                                                                                                                                                                                                                    YVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35682 MW; 39476E03FD201D6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 877; DB 11;
Pred. No. 5.2e-70;
2; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                superfamily of the mouse.";
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O1-MAR-2002 (TrEMBLrel. 20, Le

f O1-MAR-2003 (TrEMBLrel. 23, Le

f O1factory receptor MOR30-1.
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SEQUENCE
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GECRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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olfactory receptor gene superfamily of
Neurosci. 0:0-0(2002).
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Pred. No. 7.1e-70;
3; Mismatches 82
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Best Local Similarity
Matches 155; Conserv
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01-MAR-2002 (TrEMBLrel 20, I
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01factory receptor MOR10-2
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata,
Mammalia, Eutheria; Rodentia,
                                                                                                                                          SEQUENCE FROM N.A.
Zhang X., Firestein &
"The olfactory recept
Nat. Neurosci. 0:0-0
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Q8VGZ3;
01-MAR-2002 |
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#RINTS; PR00217; GFCKRHODDOSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072997; AAL60660.1; -. InterPro; IPR001064; Crystallin.
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Zhang X., Firestein S.J.;
"The olfactory receptor gene
"The olfactory occopion"
Nat. Neurosci. 0:0-0(2002).
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE
                                                                                                                              EMBL; AY072987; AAL60650.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRTHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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SEQUENCE
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Zhang X., Firestein S.J.;

"The olfactory receptor gene superfamily
Nat. Neurosci. 0:0-0(2002).
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00217; GPCRRHODOPSN
PROSITE; PS00225; CRYSTALLIN BETAGAMA;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                 Submitted (JAN-2002) to the
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                          Adams M.
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n 53.3%; So
Similarity 53.2%; Po
58; Conservative 59;
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Rodentia;
                                                                                            35357 MW;
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  Score 862.5; DB
Pred. No. 1e-68;
9; Mismatches
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                                                                                            165EC74EC379CAA7 CRC64;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00217; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50282; G_PROTEIN_RECEP_F1_2; 1.
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Zhang X., Firestein S.J.;
"The Olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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XU L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N., Sesterhenn I.A., Zou Z., Srikantan V., Augustus M., Roschke V., Carter K., McLeod D.G., Moul J.W., Soppet D., Srivastava S.; "PSGR, a novel prostate-specific gene with homology to a G protein-coupled receptor, is overaxpressed in prostate cancer."; Cancer Res. 60:6568-6572(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and genetic characterization of an evolutionarily conserved human olfactory receptor that is differentially expressed across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21564169; PubMed=11707321;
Yuan T.T., Toy P., McClary J.A., Lin R.J., Miyamoto N.G.
Kretschmer P.J.;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AF369708; AAX38728.1; -.
EMBL; AY033942; AAX57550.1; -.
EMBL; BC020768; AAH20768.1; -.
Genew; HGNC:15195; OR51E2.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004984; F:olfactory receptor activity; NAS.
GO; GO:0007608; P:olfaction; NAS.
InterPro; IFR000276; GECR_Rhodpsn.

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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

G-protein coupled receptor; Glycoprotein.

G-protein coupled receptor; Glycoprotein.

G-protein coupled receptor; Glycoprotein.

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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
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"Identification of a novel G-protein coupled receptor expressed distinct brain regions and a defined olfactory zone.";
Recept. Channels 6:141-151(1998).
-!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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TISSUE SPECIFICITY: EXPRESSED ONLY IN SOME AREAS OF THE
IN THE OLFACTORY EPITHELIUM.
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16-OCT-2001 (Rel. 40, Last sequence upda
T 15-SEP-2003 (Rel. 42, Last annotation up
EMBL; AF137396; AAG41678.1; -.

GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004884; F:olfactrory receptor activity
GO; GO:0004884; F:olfactror; NAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; pF00001; 7tm_1; 1.

PRINTS; PR00237; GFCRRHODDPSN.
PROSITE; PS00237; GFCRRHODDPSN.
PROSITE; PS00237; GFCRFOTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; G1:
Multigene family; Olfaction.
EXTRACELLULAR (P)
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                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Bulger M., Bender M.A., van Doorninck J.H., Wert
Felsenfeld G., Groudine M., Hardison R.;
"Comparative structural and functional analysis
receptor genes flanking the human and mouse beta
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Mammalia; Eutheria;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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FUNCTION: PUTATIVE ODORANT RECEPTOR.
SUBCELLULAR LOCATION: Integral membrane protein
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                 01 (Rel. 40, Created)
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03 (Rel. 42, Last annotation
receptor 5111 (HOR5'betall).
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CYTOPLASMIC (POTENTIAL)
4 (POTENTIAL)
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Pred. No. 4.5e-60
1; Mismatches 8
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CYTOPLASNIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCKAC. . .) (P.
F17CD16C95FD1AF6 CRC64;
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EXTRACELLULAR (POTENTIAL)
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SEQUENCE FROM N.A.

MEDIINE=20570519; PubMed=11121057;

Bulger M., Bender M.A., van Doorninck J.H.,

Felsenfeld G., Groudine M., Hardison R.;

"Comparative structural and functional analy

receptor genes flanking the human and mouse

clusters.";
                                       Proc. Natl. Acad. Sci.
                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                   -!- SUBCELLULAR LOCATION: Integral n
                                                                                                                                         NCBI_TaxID=9606;
entry
                                                                                                                                                    Chordata;
Primates;
                                       ODORANT RECEPTOR.
copyright.
                                                 97:14560-14565 (2000)
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                   membrane protein.
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GO; GO:0016021; C:integral to membrar
GO; GO:0004984; F:olfactory receptor
GO; GO:0007608; P:olfaction; NAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Dfam. PEND001.7 Trm 1.1
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane;

Multigene family; Olfaction.
 Olfactory receptor
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 2.7e-55;
6; Mismatches 93
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EXTRACELLULAR (POTENTIAL)

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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Bulger M., Bender M.A., van Doorninck J.H., Wertman B.,
Felsenfeld G., Groudine M., Hardison R.;
"Comparative structural and functional analysis of the creceptor genes flanking the human and mouse beta-globin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EB. European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                C. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
FUNCTION: PUTATIVE ODORANT RECEPTOR.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
activity;
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MBL outstation -
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EMBL; AF137396; AAG41676.1; GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004984; F:olfactory receptor activity
GO; GO:0004986; F:olfaction; NAS.
InterPro; IPR00276; GPCR\_Rhodpsn.
Pfam, PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1 1; 1.
PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1 2; 1.
G-protein coupled receptor; Transmembrane; G1
Multigene family; Olfaction. ; Score 792.5; ; Pred. No. 3.36 71; Mismatches CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL). CYTOPLASMIC (P BY SIMILARITY. N-LINKED (GLCN 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL). EXTRACELLULAR
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                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHCDOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
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GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0004984; F:olfactory receptor activit

GO; GO:0007508; P:olfaction; NAS.
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Mammalia; Eutheria;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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    (Human)
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PUTATIVE ODORANT RECEPTOR.
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41, Last sequence up
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11, Simi (HOR5'beta7).
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    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane;
Multigene family; Olfaction.
                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              Puchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R., Shmulavich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U., Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R., "DEFOG: a practical scheme for deciphering families of genes."; submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
-!- SUBCELLULAR LOCATION: INtegral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Mammalia; Eutheria;
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DT 15-SEP-2003 (Rel. 42, Last annotation update)

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                                                       MEDIINE=20570519; PubMed=11121057; Bulger M., Bender M.A., van Doorninck J.H., Felsenfeld G., Groudine M., Hardison R.; "Comparative structural and functional analy receptor genes flanking the human and mouse clusters.";
                                                                                                                                                                                                                      MEDLINE=99443868; PubMed=10512676; Reingold E.A., Penny L.A., Nienhuis A.W., Forget B.G.; Reingold E.O., receptor gene is located in the extended human globin gene cluster and is expressed in erythroid cells."; Genomics 61:15-23(1999).
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FUNCTION: PUTATIVE ODORANT RECE
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Primates;
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BY SIMILARITY.
N-LINKED (GLCN
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL)
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7; Mismatches
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                         97:14560-14565(2000).
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                          RECEPTOR
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  membrane protein
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RESULT
OXB2\_HC
ID OX
AC QS
DT 16
DT 16

OXB2\_HUMAN STANDARD; PRT; 312 AP 99Y5P1; Q96RD4; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)

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CARBOHYD
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TRANSMEM
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EMBL; AF289204; AAG42367.1; -.
Genew; HGNC:8318; OR52A1.
GO; GO:00005887; C:integral to plasma membrane;
GO; GO:0007608; P:olfaction; TAS.
GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a control of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane;
Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                     SEQUENCE
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                                          196
 256
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                    254
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                                                                                                                                                                                                    16
                                                                                                                                                       76
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                                                                                                           TVLTLPRVTKIGVAAVVRGAALMAPLPVFIK-QLPFCRSNILSHSYCLHQDVMKLACDDI
                                                                                                                                                 STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHA
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LLAFFSFFTHRFGSHIPPYIHILFSSIYLLVPPFLNPLVYGAKTTQIRIHVVKMF
                                          QVNKIYGLEVAETVAGEDLIETIILSYIQIEITVERLEQKEAREKAENTCIAHICVELQEY
                                                             RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTÇVSHVÇAVFIFY
                                                                                       NIFTHQLVIQIGTMVVLRAAILVAPCLVLIKCRFQFYHTTVISHSYCEHMAIVKLAAANV
                                                                                                                                 SSIMPKMLGIFWENVPEIXEDSCLLQMWFIHTLQGIESGILVAMALDRYVAICXPLRHA
                   VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLF
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BY SIMILARITY.
N-LINKED (GLCN
                                                                                                                                                                                                                        Score 751; DB 1;
Pred. No. 5.le-51;
B; Mismatches 94
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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2 (POTENTIAL
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Query Match
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EMBL; AF395503; AAK94988.1; -.
Genew; HGNC:14703; OR51B2.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004984; F:olfactory receptor activity; NAS.
GO; GO:0007508; P:olfaction; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-99238494; PubMed=10220430;

MUSINE-99238494; PubMed=10220430;

Bulger M.A., van Doorninck J.H., Saitoh N., Telling A.,

"Conservation of sequence and structure flanking the
beta-globin loci: the beta-globin genes are embedded
of odorant receptor genes.";

Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134(1999).
                                   DISULFID CARBOHYD
                                                                                                        TRANSMEM
DOMAIN
                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
Multigene family; Olfaction.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bulger M., van Do
Bender M.A., Fels
Proc. Natl. Acad.
                         SEQUENCE
                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Mammalia; Eutheria;
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Olfactory re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                    requires a
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A., Felsenfeld (
Acad. Sci. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
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r 51B2 (HO
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Primates;
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CYTOPLASMIC (F
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Catarrhini; Hominidae;
                      LINKED (GLCNAC. . .) (I
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                                                                                                                                                                                                                         G-protein
Multigene
DOMAIN
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-i- FUNCTION: PUTATIVE ODORANT RECEPTOR.
                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane;

Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (Secons send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute.
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    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTBIN COUPLED RECEPTORS.

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eceptor 52E6.
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Best Local
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SEQUENCE FROM N.A.
MEDLINE=99238494; PubMed=10220430;
MEDLINE=99238494; PubMed=10220430;
Melger M., van Doorninck J.H., Saitoh N., Telling A.,
Bender M.A., Felsenfeld G., Axel R., Groudine M.;
"Conservation of sequence and structure flanking the beta-globin loci: the beta-globin genes are embedded of odorant receptor genes.";

Natl. Acad. Sci. U.S.A. 96:5129-5134(1999).
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Q9Y5P0;
16-OCT-2001
16-OCT-2001
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                        receptor genes flanking clusters.";
                                                                                                                                                                                                                        Bulger M., v
Bender M.A.,
                                                                MEDLINE=20570519; PubMed=11121057;
Bulger M., Bender M.A., van Doorni
Felsenfeld G., Groudine M., Hardis
"Comparative structural and functi
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01 (Rel. 40, Last sequence update)
03 (Rel. 42, Last annotation updat receptor 51B4 (HOR5'betal).
                                                                                                                                                                                                  van Doorninck J.H., Saitoh N., Telling
., Felsenfeld G., Axel R., Groudine M.;
. Acad. Sci. U.S.A. 96:8307-8307(1999).
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Primates;
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, Hardison R.;
d functional analy
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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DOMAIN
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ew; HGNC:14708; OR51B4.
GO:0016021; C:integral to membrane; NAS.
GO:0004984; F:olfactory receptor activity;
                                                                                            184
304
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                                            CVLVFHITVMGLSFIHRFGKHAPHVVPITMSYVHFLFPPFVNPIIYSIKTKQIQRSIIRL
                                                                                                                                            RTPLRYNCILTNSRVMNIGLGVLMRGFMSILPIILSLYCYPYCGSRALLHTFCLHQDVIK
                                                                                                                                                                  CHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMK
                                                                                                                                                                                           ADTDLGMTFTTMPTVLGVLLLDQREIAHAACFTQSF-
                                                                                                                                                                                                                SGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAI
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                                                                                                                                                                                                                                                              SSATYFILIGLEGLEEAQEWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEEMYIFLCML
                                                                    AVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRL
                                                                                            LACADITENHIYPIIQTSLTVFLDALIIIESYILILKTVMGIASGQEEAKSLNTCVSHIS
                                                                                                                  LACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVC
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40.5%;
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                                                                                                                                                                                                                                                                                       Score 632; DB
Pred. No. 7.4e
72; Mismatches
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BY SIMILARITY N-LINKED (GLCN
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3 (POTENTIAL).
CYTOPLASMIC (P
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1 (POTENTIAL).
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Q9NQNT;

16-OCT-2001 (Rel. 4

16-OCT-2001 (Rel. 4

15-SEP-2003 (Rel. 4
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InterPro; 1rav.

Pfam; PF00001; 7tm 1; 1.

PROUTER PRO0237; GFCRENODOPSN.

PROSITE; PS00237; G_PROTEIN RECEP F1 2; 1.

PROSITE; PS00237; G_PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;

G-protein coupled receptor; Transmembrane; GPTENTIAL).

G-protein coupled receptor; Transmembrane; GPTENTIAL).
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DOMAIN
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DOMAIN
                                                                                                                                                                DISULFID CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
        122
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                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:8276;
                                                                                                                  Similarity 35.2
l3; Conservative
       DRYVAICNPLRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAI-OLPFCGDNVINHFTC 180
                                           FFLGNLSFLDICFTTSSVPLVLDSFLTPQETISFSACAVQMALSFAMAGTECLLLSMMAF
                                                            IFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAF 122
                                                                                                NESSATY-FILIGI----PGLEEAQFWLAFFLCSLYLIAVLGNLTIIYIVRTEHSLHEPMY
                        DRYVAICHPLRHATVLTLPRVTKIGVAA-VVRGAALMAPLPVFIKQLPFCRSNILSHSYC 181
                                                                               NETSPVMGFVLLRLSAHPELEKTFFVL---ILLMYLVILLGNGVLILVTILDSRLHTPMY
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Last annotation update)
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                                                                                                                   64;
                                                                                                                  Score 464; DB 1; L
Pred. No. 6.6e-29;
4; Mismatches 111;
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602602FCA96A179F CRC64;
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                                                                                                                   Gaps
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DISULFID
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane;
                                                                                                                                                              TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M84005; AAA39862.1; -.
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Mammalia; Eutheria;
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Dionne V.E., Heinemann S.F.;
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(Rel. 32, Last sequence update)
(Rel. 36, Last annotation update)
sceptor 15 (OR3).
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                              Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                              family.
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (P.
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(See http://www.isb-sib.ch/announce/
(GLCNAC. . .) (POTENTIAL)
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Best Local
EMBL; M6439; AAA41754.1; -.

PIR; I33701; I23701.

InterPro; IPR00076; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN_COUPLED (G_PROTEIN_RECEP_F1_2); 1.

Multigene family; Olfaction.

Multigene family; Olfaction.

EXTRACELLULAR (POTENTAL).
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P23273;
                                                                                                                                                                                    use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence up
01-JUL-1993 (Rel. 26, Last annotation
Olfactory receptor-like protein I14.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a copyrent of the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the Thomas of the content is used by non-profit institutions as long as its content is used by non-profit.
                                                                                                                                                                                                                                                                                                                                                                                              Buck L., Axel R.;
"A novel multigene family may encode odorant receptors: a molecular basis for odor recognition.";
Cell 65:175-187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91191556; PubMed=1840504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: OLFACTORY EDITHELIUM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Matches
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         MEDIJINE-9063798; PubMed=9847080;
Centola M., Chen X., Sood R., Deng Z., Aksentijevich I.
Ricke D., Chen X., Wood G., Zaks N., Richards N., Krizm
Mansfield E., Apostolou S., Liu J., Shafran N., Vedula
Cercek A., Kahan T., Gumucio D., Callen D.F., Richards
Cercek R.K., Doggett N.A., Collins F.S., Liu P.P.,
Fischel-Ghodsian N., Kastner D.L.;
"Construction of an approximately 700 kb transcript map
familial mediterranean fever locus on human chromosome
Genome Res. 9:1-21(1998).
                                                                                                                                                                                                                                                                                                                        -02C1 HUMAN
095371;
16-0CT-2001
16-0CT-2001
16-0CT-2001
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Mammalia; Eutheria;
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                                                                                                                                                                                      SEQUENCE FROM N.A.
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 FUNCTION:
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L (Rel. 40, L
ceceptor 2C1
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 PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Primates;
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33.5%;
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EXTRACELLULAR
5 (POTENTIAL).
CYTOPLASMIC (P
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N-LINKED (GLCNAC. . .)
BY SIMILARITY.
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EXTRACELLULAR
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on update)
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Best Local Similarity 33.4%;
Matches 102; Conservative 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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DOMAIN
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Olfaction.

DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF098664; AAC83557.1; -.
Genew; HGNC:8242; OR2C1.
GO; GO:0004984; F:olfactory receptor activity; TAS.
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PRINTS; PR00237; GPCRRHODOPSN.
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Pfam; PF00001; 7tm_1; 1.
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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300 ALRKL 304
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                                                                                                                     SHVCAVFIFY-VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ 302
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                                        RILRL 307
                                                                                 SHLLVVFLFYGSASYGYLLPAKNSKQDQGK---FISLFYSLVTPMVNPLIYTLRNMEVKG 299
                                                                                                                                                                                                                                                                 AVCRPIRYTAIMNPQICWILAVIAWIGGIGNSVIQSTFTIQIPICGHRRVEGFICEVPAM 184
                                                                                                                                                                                                                                                                                                          AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKOLPFCRSNILSHSYCLHODV 186
                                                                                                                                                                          IKLACGDTSLNQAVLNGVCTFFTAVPLSIIVI--SYCLIAQAVLKIHSAEGRRKAFNTCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34506 MW;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
; CC4D7D349BE8B9E7 CRC64;
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
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Search completed: February 9, 2004, 16:24:16
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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285.5	289.5	303.5	310.5	313.5	366	368.5	370	375	379.5	383	383.5		86.	•	390.5
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RESULT 2 E45774 cdorant receptor 8 - channel catfish c)Species: Ictalurus punctatus (channel catfish) C;Species: Ictalurus punctatus (channel co-Feb-195 #text_change 26-Aug-1999 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 C;Accession: E45774 R;Ngai, J:, Dowling, M.M.; Buck, L.; Axel, R.; Chess, A. Cell 72, 657-666, 1993 genes encoding odorant receptors in the channel catfish. A;Reference number: A45774; MUID:93201590; pMID:7916654 A;Accession: E45774	Db 261 CVFLQFYLLAFFSFTHRFGSH	76 STSSMPKMLAIFWFNSTTIQEDACLLQIFAIH-SLSGMESTVLLAMAFDRYVAI	Query Match  34.1%; Score 552; DB 2; Length 292;  Best Local Similarity 40.3%; Pred. No. 2.2e-41;  Matches 114; Conservative 49; Misatches 88; Indels 32; Gaps 6;  Qy  16 LIGLPGLEBAQFWLAFPLCSLYLIAVIGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI 75  Qy  1	RESULT 1 A60547 A60547 hypothetical protein (HPFH breakpoint 3' region) - human (fragment) hypothetical protein (HPFH breakpoint 3' region) - human (fragment) N;Alternate names: olfactory receptor homolog C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Caccess: 10-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999 C;Accession: A60547; A60482 R;Feingold, E.A.; Forget, B.G. Blood 74, 2178-2186, 1899 A;Title: The breakpoint of a large deletion causing hereditary persistence of fetal hemo A;Reference number: A60547; MUID:90028751; PMID:2478223 A;Molecule type: DNA A;Residues: 1-292 <fei>C;Superfamily: olfactory receptor OR14</fei>	35 383 23.7 333 2.701 Olfactory receptor 36 379.5 23.5 327 2 F23701 Olfactory receptor 37 375 23.2 317 2 D23701 Olfactory receptor 38 370 22.9 315 2 D23701 Olfactory receptor 39 368.5 22.8 315 2 JC4658 Olfactory receptor 40 366 22.6 318 2 JC5202 Olfactory receptor 41 313.5 19.4 234 2 S29000 Olfactory receptor TB64 42 310.5 19.2 22 B40745 Olfactory receptor of 43 303.5 18.8 264 2 PC4369 Olfactory receptor Olfactory receptor 44 289.5 17.9 234 2 S28999 Olfactory receptor 45 285.5 17.7 222 2 D40745  ALIGNMENTS

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RESULT 3
S29710
olfactory receptor OR18 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29710
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstar
Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PMID:7678922
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A;Note: sequence extracted from NCB1 backbone (NCBIP:127748)
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; transmembrane protein
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A; Residues: 1-307 < RAM>
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A;Molecule type: mRNA
A;Residues: 1-313 <NGA>
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FGTCVSHVCAVFIFYVP--FIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVK
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                                                                       --TYFIGLTVIANGGVNCIVIFTLLLG-SYGIILRSLKTQSQEGRRKA
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Pred. No. 1.4e-32;
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Ceil 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors:
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: I23701
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22
C;Accession: I23701
P,Buck T
                       A;Cross-references: GB:M64391; NID:g205843; PIDN:AAA41754.1; PID:g205844 C;Superfamily: olfactory receptor OR14 C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-312 < BUC>
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RESULT 4
A46247
A46247
AFACTORY receptor OR3 - mouse
C!Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession. A46247
R;Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinveron, Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A;Title: Spatial pattern of receptor expression in the olfactory epithelium.
A;Reference number: A46247; MUID:93028384; PMID:1384038
A;Accession: A46247
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-312 <NEF>
A;Cross-references: GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154
A;Note: sequence extracted from NCBI backbone (NCBIP:115362)
C;Superfamily: olfactory receptor OR14
GRRKAFNTCVSHLVVVFLFYG----SAIYGYLLPAKSSNQSQGKFISLFYSVVTPMVNP
                                                                                                                                                                                                                                                                                                                                                                                            AMAFDRYVAICHPLRHATVLTLPRVTKIGVAAV--VRGAALMAPLPVFIKQLPFCRSNIL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLL 118
                                                                           AQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRF---SKRRDSPLPVILANIYLLVPPVLNP
                                                                                                                                                      DNFLCEVPAMIKLACGDTSLNEAVLNGVCTFFTVVPVSVILV--SYCFIAQAVMKIRSVE
                                                                                                                                                                                                                                 SHSYCLHQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TRE 233
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KRALIRV 302

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RESULT 6
E23701
C1Sactory receptor I3 - rat
C1Species: Rattus norvegicus (Norway rat)
C1Species: Rattus norvegicus (Norway rat)
C1Species: Rattus norvegicus (Norway rat)
C1Species: Rattus norvegicus (Norway rat)
C1Species: Rattus norvegicus (Norway rat)
C1Species: Rattus norvegicus (Norway rat)
R1Suck, L1; Axel, R.
Cell 65, 175-187, 1991
Cell 65, 175-187, 1991
A)Ficher Rancel multigene family may encode odorant receptors: a molecular basis: A)Ficher number: A23701, MUID:91191556; PMID:1840504
A)Ficher Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel Rancel
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A; Residues: 1-310 < BUC>
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Matches 105
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Best Local S
Matches 102
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                      RORILRL 307
                                                                                                                                                                                                                                       LHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFG
                                                                                                                                                                                                                                                                                             YVAICFPLHYTSIMS-PKLCTCLVLLLWMLTTSHAMMHTL--LAARLSFCENNVVLNFFC
                                                                                                                                                                                                                                                                                                                                                YVAICHPLRHATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYC
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                                                                                 TCGSHLSVVSLFYGTIIGLYLCP--AGNNSTVKEMVMAMMYTVVTPMLNPFIYSLRNRDM
                                                                                                                                  TCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI 300
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Pred. No. 6e-31;
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R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M. Biochem. Biophys. Res. Commun. 237, 283-287, 1997
A;Title: Molecular cloning and chromosomal mapping of olfactory A;Reference number: JC5624; MUID:97415789; PMID:9268701
A;Contents: Testis
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C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
C;Accession: JC5624; S58003
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A; Molecule type: mRNA
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C; Function:
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A; Residues: 126-282 < VAW >
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olfactory receptor OR12 -
C;Species: Rattus norvegic
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Matches .102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFLSNLSFADICVTSTTIPKWLMNIQTQNKVITYIACLMQMYFFILFAGFENFLLSVMAY 120
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                                                                                                                                                                                                                                                                      FSTCASHLSVVSLFYGAILGVYL--SSAATRNSHSSATASVMYTVVTPMLNPFIYSLRNK
                                                                                                                                                                                                                                                                                                                      FGTCVSHVCAVFIFYVFFIGLSMVHRFSKRRDSFLFVILANIYLLVFFVLNFIVYGVKTK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
     norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.6%;
                            rat
     (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 430.5; DB 2;
Pred. No. 1.4e-30;
71; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:92792018
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                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
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                                                                                                                                                                                                                                                                            295
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Query Match Best Local Similarity 29.4%; Score 428; DB 2; Length 328; Best Local Similarity 29.4%; Dred. No. 2.4e-30; Matches 92; Conservative 76; Mismatches 127; Indels 18; Gaps 7;  Qy 4 PNGNESSATYFILIGLEGLEEAQFWL-AFFLCSLYLIAVIGNLTIIYIVRTEHSLHEPMY 62	RESULT 9 G45774 odorant receptor 202 - channel catfish C;Species: Ictalurus punctatus (channel catfish) C;Species: Ictalurus punctatus (channel catfish) C;Dete: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998 C;Accession: G45774 R;Ngai, J; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A. Cell 72, 657-666, 1993 A;Title: The family of genes encoding odorant receptors in the channel catfish. A;Reference number: A45774; MUID:93201590; PMID:7918654 A;Accession: G45774 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Mesidues: 1-328 <nga> A;Experimental source: olfactory epithelium A;Note: sequence extracted from NCBI backbone (NCBIP:127746) C;Superfamily: olfactory receptor OR14 C;Keywords: olfaction; transmembrane protein</nga>	Qy  7 NESSATYFILIGLPGLEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIF 64    :	C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998 C;Accession: S29708 R;Raming, K; Krieger, J; Strotmann, J; Boekhoff, I; Kubick, S; Baumstark, C; Breer Nature 361, 353-356, 1993 A;Title: Cloning and expression of odorant receptors. A;Reference number: S29707; MUID:93149273; PMID:7678922 A;Accession: S29708 A;Molecule type: mRNA A;Residues: 1-312 <ram 1.7e-30;="" 119;="" 17;="" 31.7%;="" 6;<="" 75;="" 98;="" c;superfamily:="" conservative="" dest="" gaps="" indels="" local="" match="" matches="" mismatches="" no.="" olfactory="" or14="" pred.="" query="" receptor="" similarity="" th=""></ram>
RESULT 11 A37286 Olfactory receptor I15 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999 C;Accession: A37286 R;Buck, L.; Axel, R. Cell 65, 175-187, 1991 A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Accession: A37286	67 65 127 125 184 182 238 237 297	RESULT 10 S20572 olfactory receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999 C;Accession: S20572 R;Cancession: S20572 R;Parmentier, M; Libert, F; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.; Nature 355, 453-455, 1992 A;Title: Expression of members of the putative olfactory receptor gene family in mammali A;Reference number: S20571; NUID:92131132; PMID:1370859 A;Cacession: S20572 A;Status: preliminary A;Accession: S20572 A;Status: preliminary A;Accession: S20572 A;Cacession: S20572 A;Cacession: S20572 A;Cacession: S20572 A;Cacession: S20572 A;Cacession: S20572 A;Cacession: S20571; NUID:92131132; PMID:1370859 A;Cacession: S20572 A;Cacession: S20571; NUID:92131132; PMID:1370859 A;Cacession: S20572 A;Cacession: S20571; NUID:92131132; PMID:1370859 A;Cacession: S20571; NUID:92131132; PMID:137085	Db 122 DRYVAVCNPLRYVNIVKESTILGLCVVSWLLAEPTVLTTVIRATSLPYCASNTVIQCYCD 181  Qy 183 HQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKA 238

Qy 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHBPMYIF 64    : :   :   :	RESULT 12 S29707 olfactory receptor OR5 - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Accession: S29707; B37286 R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer Nature 361, 353-356, 1993 A;Title: Cloning and expression of odorant receptors. A;Reference number: S29707; MUID:93149273; PMID:7678922 A;Recicule type: mRNA A;Residues: 1-314 <ram> R;Buck, L.; Axel, R. Cell 65, 175-187, 1991 A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:91191556; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504 A;Reference number: A23701; MUID:93149273; PMID:1840504</ram>	A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mENA, A;Residues: 1-314 -SUC- A;Cross-references: GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846 C;Superfamily: olfactory receptor OR14 C;Keywords: G protein-coupled receptor; transmembrane protein Query Match Smilarity 26.3%; Score 455.5; DB 2; Length 314; Best Local Smilarity 33.2%; Pred, No. 3.8e-30; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9; Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;  Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9
RESULT 14 \$29711 \$29711 S19711 19711 S1971 S19711 S19711 S19711 S19711 S19711 S19711 S19711 S19711 S19711 S	Query Match  Best Local Similarity 32.4%; Pred. No. 1.1e-29;  Matches 101; Conservative 63; Mismatches 127; Indels 15; Gaps 6;  Oy 9 SSATYFILIGLEGLEEAOFWLAFFLCSLYLIAVIGNLTIIVVRTEHSLHEPMYI 63  14 TNATETRESTFYITCLYNIPHAKYYYLF-LCFVYTVTFLGNSFINGTIYLARSLHTAKYI 72  OY 64 FLCMLSGIDILISTSSMEKMLAIFWENGTIQDDACLLQIFAIHSLSGMESTVLLAMAFD 123  OY 124 RYVALCHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH 183  OY 124 RYVALCHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH 183  OY 184 QDVMKLACDDRINNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAF 239  OY 184 QDVMKLACDDRINSIMGNVCTATLLYFPLILIASYVCIGFALQKIAHGVEQVKAM 249  OY 240 GTCVSHVCAVFIFYVPFIGLSMVHFFSKRDSPLPVILANIYLLVPPVLNPIVYGVKTKE 299  OY 240 GTCVSHVCAVFIFYVPFIGLSMVHFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKE 299  OY 300 IRQRILLYHIS 300  OY 300 IRQRILLYHIS 300	Qy  125 YVAICHPLEHATVLTIPRVTKIGVAAVVRGAALMAPL-PVFTKQLFCRSNILSHSY 180  123 YVAICHPLEHAMSINSPKICVSIVVLSWVITTFHAMSIHTILMARLSFCEDNVIPHF 178  Qy  181 CLHQDYMKLACEDTRVNVYGLIVIISAIGLDSLLISFSYLLIKTVLGI-TREAQAKAF 239  179 CDMSALLKLACEDTRVNVYGLIVIISAIGLDSLLISFSYLLIKTVLGI-TREAQAKAF 239  QY  240 GTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLFVILANIYLLVPBVLNPFIYSHRNED 296  QY  240 GTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLFVILANIYLLVPBVLNPFIYSHRNED 296  QY  300 IR 301  RESULT 13  RESULT 14  RESULT 14  RESULT 15  RESUL

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GAT>
A;Cross references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1;
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A;Description: Olfactory receptor proteins: expression, charact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51356; S47014
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1188, 1994
A;Title: Olfactory receptor proteins. Expression, characterization and partial purificat
A;Reference number: S51356; MUID:95045546; PMID:7957207
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C;Species: Rattus norvegicus (Norway rat)
C;Datecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51356; 847014
C;Accession: S51356; 847014
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A;Molecule type: mRNA
A;Residues: 1-309 <GA2>
A;Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1;
C;Superfamily: olfactory receptor OR14
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A;Reference number: 829707; MUID:93149273; PMID:7678922
A;Accession: 829711
A;Molecule type: mRNA
A;Residues: 1-305 <RAM>
                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S47014
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Best Local
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Best Local
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                          66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125
                                                                                                                                                                               104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                               25.9%; Score 418.5; DB 1; Similarity 33.0%; Pred. No. 1.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 25.9%; Score 418.5; DB 2;
Similarity 32.5%; Pred. No. 1.5e-29;
30; Conservative 62; Mismatches 115;
SSLSFVDLCYSTVITEKMLUNFLGKKNFITYSECMAOFFFFAIFVVTEGYLLTVMAYDRY 124
                                                                                     GNHSAVVVEVLVGLTKQPELLLPLFFLFLVIYVLTVVGNLGMILLIIVSPLLHTPMYYFL
                                                                                                               GNESSATYFILIGLEGLEEAQFWLAFELCSLYLIAVLGNLTIIYIVRTEHSLHEEMYIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKDVKAAV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKEIRQRI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTVVVIFYGTIFSM-----YAKPKSQDLTGKDKFQTSDKIISLFYGVVTPMLNPIIYSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCAVFIFYVPFIGLSMVHRFSKRRDSPL-----PVILANIYLLVPPVLNPIVYGVK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTTSSVPSTLVSLISKKRNISFSGCTVQMFVGFAMGSTECLLLGMMAFDRYVAICNPLRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISTSSMPKMLAIFWENSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIGLSGYPKTEILYFVIVLVMYLVIHTGNGVLIIASIFDSHLHTPMYFFLGNLSFLDIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILIGLEGLEEAQFWLAFFLCSLYLIAVLGNLTIIYIVRTBHSLHEEMYIFLCMLSGIDIL 74
                                                                                                                                                                               Conservative
                                                                                                                                                                            63;
                                                                                                                                                                            Mismatches 119; Indels 29;
                                                                                                                                                                                                                  Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      characterization and partial
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                               VYGVKTKEIRQRILR 306
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Search completed: February 9, 2004, 16:25:43 Job time : 21 secs

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US-09-439-313-526
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILLING DATE: 1999-11-12
RUMBER OF SEQ ID NOS: 575
SOFTWARE: RastSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
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Fanger, Gary
Retter, Mark
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RESULT 2
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GENERAL INFORMATION:
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APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HP
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, C
ADDRESSEE: STUART & OLSTEIN
APPLICATION NUMBER: 1
FILING DATE: 06-JUN-
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMAT
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STREET: b ...
CITY: Roseland
CTATE: New Jersey
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                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COUNTRY: U
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        INFORMATION:
                                            06-JUN-1995
                                                               US/08/465,980
                                                                                                       Version
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REGISTRATION NUMBER: 36,134
REFERENCE, DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-994-1700
TELEFAX: 201-994-1704
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
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Best Local
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FEATURE:
NAME/KEY: CDS
LOCATION: 274
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Similarity 64.4%;
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    CTATGTGCCACTTATTGGCCTCTCAGTTGTACACCGCTTTGGAAACAGCCTTCATCCCAT
                                         CTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCC
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                                                                                 GTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTCACACATTGGTGTGGTACTCGCCTT
                                                                                                                         ACTTCTCATCTCTCATATCTGCTTATTCTTAAGACTGTGTTTGGGCTTGACACGTGA
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Pred. No. 7.7e-81;
0; Mismatches 314;
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RESULT 3
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                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 574; Conserv
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-UNY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1474 base pairs
TYPE: nucleic acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 36,1
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    TGAGCACAGCCTGCATGAGCCCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACAT 350
                                      CCTTTCCATGTATGTAGTGGCAATGTGTGGAAACTGCATCGTGGTCTTCATCGTAAGGAC
                                                                          GTGCTCCTCTACCTTATTGCTGTGCTAGGTAACTTGACATCATCTACATTGTGCGGAC
                                                                                                                 CTGTGTGCTTATTGGTATCCCCAGGATTAGAGAAAGCCCATTTCTGGGTTGGCTTCCCCCCT
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Li, Yi
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274.,1233
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                                                                                                                                                                                       Score 372.6; DB 2;
Pred. No. 7.7e-81;
0; Mismatches 314;
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                                                                                                                                                                                                                              Length 1474;
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APPLICANT: Soppet,
APPLICANT: Li, Yi
APPLICANT: Rosen,
APPLICANT: Ruben,
                                                                                                                                                                                                                                                                                                                                         Sequence 1,
                                                                                                                                                                                                                                                                                                                        Patent No.
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                 APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: BAIN, GILFILLAN, CECCHI
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI
                                                      COUNTRY:
                                                                        CITY: Roseland
STATE: New Jersey
                                                                                                                                   ADDRESSEE:
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                                                                                                             BE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
JE: STUART & OLSTEIN
6 Becker Farm Road
                                                        USA
                                                                                                                                                                                                                                                                                Soppet, Daniel R
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Best Local Similarity
Matches 574; Conserv
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TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/339,115
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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CACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTCATGGGCGTGGACGT
                                TATCCGGGTCAATGTCGTCTATGGCCTTATCGTCATCATCTCCGCCATTGGCCTGGACTC
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                                                                                                                                          CGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGCTGGCCTTCTGCCACTC
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                                                                    CAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAAGTTGGCCTATGCAGA
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                                                                         PCT-US95-07093-1
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Query Match 11.9%;
Best Local Similarity 64.4%;
Matches 574; Conservative
                                                                                                                                                                                                                                                    TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
                                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: DATA: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CARELLA, BYRNE, BAIN, ADDRESSEE: STUART & OLSTEIN
                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 TGTGCGTGTTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAATCCCATCAT 1142
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   Score 372.6; DB 5;
Pred. No. 7.7e-81;
0; Mismatches 314;
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RESULT 6
US-09-668-680-13
                                                            Patent No. 6436703;
GENERAL INFORMATION;
APPLICANT: Tang, Y.
APPLICANT: Liu, Cher
APPLICANT: Zhou, Pi
                                                                                                                                                                      Sequence
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APPLICANT:
APPLICANT:
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o. 6436703
Tang, Y. Tom
Liu, Chenghua
Zhou, Ping
Asundi, Vinod
Zhang, Jie
Wang, Jian-Rui
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APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Aci
TITLE OF INVENTION: No. 6436703el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790C1P2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
SEQ ID NOS: 13
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Best Local Similarity 57.6%;
Matches 511; Conservative
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ORGANISM: Homo :
FEATURE:
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CAAGGCATTTGGCACTTGCGTCTCATGTGTGTGCTGTTTCATATTTCTATGTACCTTT
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                                                                CATTTCCTATGGCTTTATCCTCCATGCAGTCTTTCACCTTCCATCATGATGCCCCAGCA 1295
                                                                                                 CTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACA---CGTGAAGCCCAGGC
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Pred. No. 3e-54;
0; Mismatches 370;
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; ORGANISM: Homo sapiens
US-09-439-313-462
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                                                                                                                                  US-09-352-616A-462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DBY, CRAIG
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION UNMERS: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 462
LENGTH: 231
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICAT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
APPLICANT: Head, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Kalos, Michael
                                                                                      Sequence 462, Application US/09352616A Patent No. 6395278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1745 GTACCCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGG 1804
                                                                                                                                                                                                                                               1925 TCTAGAGGAGGTATTTAATTTCTTCTCACTCATCCAGTGTTTGTATTTAGGA 1975
                                                                                                                                                                                                                                                                                                                                    1865 GAAGAACTGTTAGAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1416 CTTTCTGGCTAATCTCTATGTGCTGGTGCCTCCTGTACTCAATCCTATTCTCTATGGAGC
                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 CATTGGATTGTCCATGGTGCATCGCTTTAGCAAGCGGCGTGACTCTCCGC---TGCCCGT
                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                        GTCATGCAAGTATAAAAATT - AAAAAAAAAAAAAACACTTCATGCCCAATCTCATATGATGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                               GTCATACAAGTATAAAAATTAAAAAAAAAAAAAAAAGACTTCATGCCCAATCTCATATGATGTG 1864
                                                                                                                                                                                                                                                                                                      GAAGAACTGTTAGAGAGACCCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTACCCTCATTGTAGCCATGGGAAAATTGATGTTCAGTGGGGATCAGTGAATTAAATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTTCTCCTCACCCÁCCGCTTTGGTCÁCCACGAAGTCCCCCAAGCATGTGCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGCTCTGAGTACCTGTGGCTCCCACATTGGCATCATCCTGGTTTTCTACATCCCTGC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retter, Mark
Solk, John
Day, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanger, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09439313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 215.4; DB 4;
Pred. No. 4.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 231;
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SOFTWARE: FastSEQ for Wi
SEQ ID NO 462
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-462
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Patent No. 6500938
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Best Local Similarity 98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/9/352,616A
CURRENT FILING DATE: 1999-07-13
             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: PATHMAY GENE
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               APPLICATION NUMBER: U. FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3174 PORTER DRIVE
845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSITION FOR THE DETECTION PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                          US/09/016,434
                                                             PA-0002
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Pred. No. 4.3e-43;
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RESULT 10
US-09-016-434-1312
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                                         CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1312:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Satent No. 6500938
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNTUT01
CLONE: 998550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Janice Au-1011
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Useffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION F
TITLE OF INVENTION: PATHWAY GENE
TITLE OF TENTENCES: 1490
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALTURE
TYPE: r
                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: HEREW CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                        APPLICATION NUMBER:
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            1854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                            PA-0002 US
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Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR THE DETECTION EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 234;
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; STRANDEDNESS: sing; TOPOLOGY: linear; immediate source; LIBRARY: GENBANK; CLONE: 932085
US-09-016-434-1312
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Pred. No. 6.3e-23;
0; Mismatches 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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LIBRARY: GENBANI
CLONE: g1041044
-09-016-434-1056
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 105
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: HEREWIT CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
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579
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                                                             TGGACCTCTGTTTCACCACGAGTTGTGTTCCCCCAAATGCTGGCCAACCTCTGGGGCCCAA 758
                                                                                                                                                                                                                           TGGATGTCATCACTTCCTACCTCCTAACCCTAGTGGGCAACACACTCATCATCCTGCTGT 638
                                                                                                                                                                                                                                                                     TCCCATTGTGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACAATCATCTACATTG 283
                                                                                                                                                                                                                                                                                                             CACCGGGCTTCCTCCTTCTGGGCTTCTCTGAACACCCCAGGGCTGGGAAGGACTCTCTTCG 578
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Pred. No. 9.9e-21;
0; Mismatches 480; Indels
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US-08-467-948A-1
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APPLICANT:
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APPLICANT:
APPLICANT:
                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
             CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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FILING DATE:
                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                     COUNTRY:
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CAO, LIAN
NI, JIAN
                                                                                                                                                                                                                                                                                                                GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                                                                         USA
06-JUN-1995
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             US/08/467,948A
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Best Local Similarity 48.0%;
Matches 378; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pair
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FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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LOCATION:
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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Pred. No. 6.9e-20;
0; Mismatches 406;
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US-08-467-947A-1
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US-08-467-947A-1
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Patent No.
GENERAL IN
                                                                                                 Query Match
Best Local Similarity
Matches 378; Conserv
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                               MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION: 202-371-2600
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CURRENT APPLICATION DATA:
US/08/467,947A
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                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: LIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0,
                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: Polynucleotides Encoding Human G-Protein TLE OF INVENTION: Coupled Receptor GPR1
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                                 137 AATCAGACAATGGTCACAGAGTTCCTCCTACTGGGATTTCTCCTGGGCCCAAGGATTCAG
                                                                 151 AATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCCCTGGTTTAGAAGAGGCTCAG 210
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 TTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCTGTGCTAGGTAACTTGACA 270
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1100 NEW YORK AVE.,
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                    Conservative
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Pred. No. 6.9e-20;
0; Mismatches 406;
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